# **WEST Search History**

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DATE: Thursday, May 12, 2005

Hide?	<u>Set</u> Name	Query	<u>Hit</u> Count
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	L1	heavychain or heavy-chain or hc or h-c or carboxyterminal or carboxylterminal or carboxyl-terminal or (receptor near3 binding) or (targeting near3 moeity) or (receptor near3 domain) or (binding near3 moeity) or (receptor near3 moiety) or rbonthc or rbont-ch or bonthc or bont-hc	54884
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	L2	heavychain or heavy-chain or hc or h-c or carboxyterminal or carboxylterminal or carboxyl-terminal or (receptor near3 binding) or (targeting near3 moeity) or (receptor near3 domain) or (binding near3 moeity) or (receptor near3 moiety) or rbonthc or rbont-ch or bonthc or bont-hc	152450
	L3	botulin or botulinum or botinolysin or botulism or botox or btox or btn or btx or neurotoxin or neuro-toxin	11128
	L4	L3 and (11 or 12)	3434
	L5	L4 and clostrid\$	1416
	L6	(11 or 12).clm. and 13.clm.	31

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DATE: Thursday, May 12, 2005

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	L6	L1 and human .	1
	L7	L1 and transgen\$	0

END OF SEARCH HISTORY

Record List Display Page 1 of 2

### **Hit List**

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Generate OACS

#### **Search Results -** Record(s) 1 through 1 of 1 returned.

1. Document ID: US <u>20030009025</u> A1

L6: Entry 1 of 1 File: PGPB

Jan 9, 2003

DOCUMENT-IDENTIFIER: US 20030009025 A1

TITLE: Recombinant vaccine against botulinum neurotoxin

#### Pre-Grant Publication (PGPub) Document Number: 20030009025

#### Summary of Invention Paragraph:

[0008] <u>Human</u> botulism poisoning is generally caused by type A, B, E or rarely, by type F toxin. Type A and B are highly poisonous proteins which resist digestion by the enzymes of the gastrointestinal tract. Foodborne botulism poisoning is caused by the toxins present in contaminated food, but wound and infant botulism are caused by in vivo growth in closed wounds and the gastrointestinal tract respectively. The toxins primarily act by inhibiting the neurotransmitter acetylcholine at the neuromuscular junction, causing paralysis. Another means for botulism poisoning to occur is the deliberate introduction of the toxin(s) into the environment as might occur in biological warfare. When the cause of botulism is produced by toxin rather than by in vivo infection the onset of neurologic symptoms is usually abrupt and occurs within 18 to 36 hours after ingestion. The most common immediate cause of death in respiratory failure due to diaphragmatic paralysis. Home canned foods are the most common sources of toxins. The most frequently implicated toxin is toxin A, which is responsible for more than 50% of morbidity resulting from botulinum toxin.

#### Summary of Invention Paragraph:

[0010] Agents that abolish the action of BoNT have been investigated since the 1940s. Early work at Fort Detrick in the 1940s lead to the development of a toxoid vaccine to protect against serotypes A, B, C.sub.1, D, and E toxins. The toxoid vaccine was manufactured by growing five Clostridium botulinum strains, extracting and precipitating the toxin from the growth media after cell lysis. Formalin was added to the crude preparation to inactivate the neurotoxin. Residual formalin was left in the vaccine product to ensure the toxin remains non-toxic. The product was adsorbed to aluminum hydroxide and blended. Currently, a pentavalent toxoid vaccine against serotypes A through E (Anderson, J. H., et al., (1981), "Clinical Evaluation of Botulinum Toxoids," Biomedical Aspects of Botulism, (Lewis, G. E., Ed.), pp. 233-246, Academic Press, New York; Ellis, R. J., (1982), "Immunobiologic Agents and Drugs Available from the Centers for Disease Control. Descriptions, Recommendations, Adverse Reactions and Scrologic Response," 3rd ed., Centers for Disease Control. Atlanta, Ga.; Fiock, M. A., et al., (1963), "Studies of Immunities to Toxins of Clostridium Botulinum. IX. Immunologic Response of Man to Purified Pentavalent ABCDE Botulinum Toxoid, " J. Immunol., 90:697-702; Siegel, L. S., (1988), "Human Immune Response to Botulinum Pentavalent (ABCDE) Toxoid Determined by a Neutralization Test and by an Enzyme-Linked Immunosorbent Assay," J. Clin. Microbiol., 26:2351-2356), available under Investigational New Drug (IND) status,

Record List Display Page 2 of 2

is used to immunize specific populations of at-risk individuals, i.e., scientists and health care providers who handle BoNT and our armed forces who may be subjected to weaponized forms of the toxin Though serotypes A, B, and E are most associated with botulism outbreaks in <a href="https://humans.put.org/">humans</a>, type F has also been diagnosed (Midura, T. F., et al., (1972), "Clostridium botulinum Type F: Isolation from Venison Jerky," Appl. MicrobioL. 24:165-167; Green, J., et al., (1983), "Human Botulism (Type F)--A Rare Type," Am. J. Med., 75:893-895; Sonnabend, W. F., et al., (1987), "Intestinal Toxicoinfection by Clostridium botulinum Type F in an Adult. Case Associated with Guillian-Barre Syndrome," Lancet, 1:357-361; Hatheway, C. L., (1976), "Toxoid of Clostridium botulinum Type F: Purification and Immunogenicity Studies," Appl. Environ. Microbiol., 31:234-242). A separate monovalent toxoid vaccine against BoNTF is available under IND status Hatheway demonstrated that the BoNTF toxoid could protect guinea pigs against a homologous challenge (Wadsworth, J. D. F., et al., (1990), "Botulinum Type F Neurotoxin," Biochem. J., 268:123-128).

#### Detail Description Paragraph:

[0063] The synthetic gene for BoNT serotype B fragment H.sub.C (see FIG. 4A) has been inserted into the yeast expression vector pHIL-D4, and integrated into the chromosome of Pichia pastoris strain GS115. The expressed product (see amino acid sequence in FIG. 4B) had the expected molecular weight as shown by denaturing polyacrylamide gel electrophoresis (PAGE) and Western blot analysis using antibodies directed against botulinum neurotoxin serotype B. The expressed recombinant BoNTB (H.sub.C) elicited high antibody titers as judged by the Enzyme Linked Immunosorbent Assay (ELISA) and, more importantly, these circulating serum titers protected mice, guinea pigs, and non-human primates from challenges with active toxin. Industrial scale manufacturing processes (fermentation and purification) have been completed and a pilot lot has been produced in compliance with cGMP.

Full	Title Citation	Front Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draws De
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Clear	Genera	ite Collection	Print	F\	vd Reis	Bkwc	Refs	Genera	ate OA	.CS
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Display Format: KWIC Change Format

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US-PAT-NO: 5939070

DOCUMENT-IDENTIFIER: US 5939070 A

TITLE: Hybrid botulinal neurotoxins

DATE-ISSUED: August 17, 1999

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE

COUNTRY

Johnson; Eric A.

Madison

WI

Goodnough; Michael C.

Stoughton

WI

Bradshaw; Marite

Madison

WI

US-CL-CURRENT: <u>424/194.1</u>; <u>424/239.1</u>, <u>435/220</u>, <u>435/842</u>, <u>514/12</u>, <u>530/350</u>, <u>530/402</u>, <u>530/412</u>, <u>530/825</u>, <u>536/23.2</u>, <u>536/23.7</u>

#### CLAIMS:

We claim:

- 1. A hybrid botulinal neurotoxin comprising:
- (a) a botulinal neurotoxin light chain; and
- (b) a botulinal neurotoxin heavy chain,

wherein the light chain and heavy chain are not of the same serotype and wherein the light and heavy chains are linked by a heterobifunctional thiol/amine linker and wherein the specific toxicity of the <a href="mailto:neurotoxin">neurotoxin</a> is at least 10.sup.6 LD.sub.50 /mg protein in vivo.

- 2. The <u>neurotoxin</u> of claim 1 wherein the heavy chain or light chain is isolated from a native botulinal neurotoxin molecule.
- 3. The <u>neurotoxin</u> of claim 1 wherein the heavy chain or light chain is obtained from a recombinant gene construct.
- 4. The  $\underline{\text{neurotoxin}}$  of claim 1 wherein the heavy and light chains are obtained from recombinant gene constructs.
- 5. A hybrid botulinal <u>neurotoxin</u> comprising light and heavy chains, which comprise botulinal <u>neurotoxin</u> catalytic, channel forming and <u>receptor binding functional domains</u>, wherein at least two functional domains are from botulinal <u>neurotoxins</u> of different serotypes and wherein the light and heavy chains are linked by a heterobifunctional thiol/amine linker and wherein the specific toxicity of the <u>neurotoxin</u> is at least 10.sup.6 LD.sub.50 /mg protein in vivo.
- 6. The <u>neurotoxin</u> of claim 5 wherein at least one of the functional domains is isolated from a native botulinal <u>neurotoxin</u> molecule.
- 7. The <u>neurotoxin</u> of claim 5 wherein at least one of the functional domains is isolated from a recombinant gene construct.

- 8. The neurotoxin of claim 5 wherein the heavy and light chains are obtained from recombinant gene constructs.
- 9. A pharmaceutical composition comprising the neurotoxin of claim 1.
- 10. A pharmaceutical composition comprising the neurotoxin of claim 5.
- 11. A method for creating a hybrid neurotoxin comprising the steps of:
- (a) isolating botulinal neurotoxin heavy and light chains from native neurotoxin molecules or a recombinant gene construct; and

linking the heavy and light chains into a hybrid neurotoxin with a heterobifunctional thiol/amine linker wherein the heavy and light chains are not of the same serotype and wherein the specific toxicity of the neurotoxin is at least 10.sup.6 LD.sub.50 /mg protein in vivo.

- 12. The method of claim 11 wherein the heavy and light chains are obtained from recombinant gene constructs.
- 13. The method of claim 12 wherein the recombinant gene constructs encode combinations of functional domains that do not occur naturally.
- 14. A hybrid neurotoxin created by the method of claim 13.

L6: Entry 23 of 31

File: USPT

Mar 30, 2004

US-PAT-NO: 6713444

DOCUMENT-IDENTIFIER: US 6713444 B1

TITLE: Buforin I as a specific inhibitor and therapeutic agent for botulinum toxin B and tetanus neurotoxins

DATE-ISSUED: March 30, 2004

#### **INVENTOR-INFORMATION:**

NAME	CITY	STATE	ZIP CODE	COUNTRY
Garcia; Gregory E.	Germantown	MD		
Gordon; Richard K.	Potomac	MD		
Moorad; Debbie R.	Rockville	MD		
Doctor; Bhupendra P.	Potomac	MD		

US-CL-CURRENT: 514/2; 424/239.1, 424/9.1, 435/252.7, 514/13, 514/21, 530/324, 530/326, 530/333, 530/344

#### CLAIMS:

What is claimed is:

1. A pharmaceutical composition for treating botulinum or tetanus toxin poisoning which comprises a biocompatible chaotrope and an endoprotease inhibiting amount of a compound selected from the group consisting of

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgAlaGlyLeuGlnPhe Pro ValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:1)

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:2),

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:3),

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgAlaGlyLeuGlnPhe Pro ValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:4) and the amidated forms thereof.

- 2. The pharmaceutical composition of claim 1, wherein the purified and isolated form is a phosphate salt.
- 3. The pharmaceutical composition of claim 2, wherein the phosphate salt is formed by the phosphorylation of Ser, Thr or Tyr.
- 4. The pharmaceutical composition of claim 1, further comprising tris-(2carboxyethyl) phosphine (TCEP).

- 5. The pharmaceutical composition of claim 1, wherein the biocompatible chaotrope is hydroxyurea or 2-oxo-1 pyrolidine acetamide.
- 6. A method for treating <u>botulinum</u> or tetanus toxin poisoning comprising administering to a subject suspected of having <u>botulinum</u> or tetanus toxin poisoning an amount of a compound for a time and under conditions effective to inhibit the toxin poisoning, wherein the compound is selected from the group consisting of

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgAlaGlyLeuGlnPhe Pro ValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:1),

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:2),

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:3),

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgGlyLeuGlnPhePro ValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:4),

ThrArqAlaArqAlaGlyLeuGlnPheProValGlyArqValHisArqLeuLeuArqLys (SEQ ID NO:5),

ThrArgLeuLeuArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:6), and the amidated forms thereof.

- 7. The method of claim 6, wherein the compound is administered to the subject prior to the subjects contact with <u>Botulinum</u> or tetanus intoxication.
- 8. The method of claim 7, wherein the <u>Botulinum</u> or tetanus intoxication results from aerosol contamination.
- 9. The method of claim 8, wherein the administration involves impregnating a filter with the compound and affixing it to the subject.
- 10. The method of claim 9, wherein the filter is a breathing filter.
- 11. The method of claim 6, wherein the compound is administered directly to a wound on the subject.
- 12. The method of claim 6, wherein the compound is conjugated to <u>botulinum</u> toxin heavy chain (Bttx-HC).

Day: Thursday Date: 5/12/2005

Time: 14:31:36

# **PALM INTRANET**

### **Application Number Information**

Application Number: 10/729122

**Assignments** 

Filing or 371(c) Date: 12/05/2003

Effective Date: 12/05/2003

Application Received: 12/08/2003 Pat. Num./Pub. Num: /20040115215

Issue Date: 00/00/0000

Date of Abandonment: 00/00/0000

Attorney Docket Number: D-

2939CIPCONDIV2

Status: 41 /NON FINAL ACTION MAILED

Confirmation Number: 9828

Oral Hearing: NO

Title of Invention: RECOMBINANT BOTULINUM TOXINS WITH A SOLUBLE C-TERMINAL PORTION, AN N-TERMINAL PORTION AND A LIGHT CHAIN

Group Art Unit: 1645 **IFW IMAGE** Class/Subclass: 424/130.100 Waiting for Response Lost Case: NO Desc. Interference Number:

Examiner Number: 72798 / PORTNER, GINNY

L&R Code: Secrecy Code:1

Unmatched Petition: NO

Third Level Review: NO Secrecy Order: NO

Status Date: 02/10/2005

**Mail Non Final** 

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Entered in Swiss-Prot in

Release 11, July 1989

Sequence was last modified in

Release 26, July 1993 Release 47, May 2005

Annotations were last modified in Name and origin of the protein

Protein name

Botulinum neurotoxin type B [Precursor]

Synonyms **EC 3.4.24.69** 

BoNT/B

Bontoxilysin B

Gene name

Name: botB

From

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Taxonomy Bacteria; I

Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

Clostridium.

### References

### [1] NUCLEOTIDE SEQUENCE.

MEDLINE=92384550; PubMed=1514783 [NCBI, ExPASy, EBI, Israel, Japan]

Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T., Minton N.P.;

"Molecular cloning of the Clostridium botulinum structural gene encoding the type B neurotoxin and determination of its entire nucleotide sequence.";

Appl. Environ. Microbiol. 58:2345-2354(1992).

[2] NUCLEOTIDE SEQUENCE OF 35-245.

**STRAIN**=Type B / NCTC 7273;

Szabo E.A., Pemberton J.M., Desmarchelier P.M.;

Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

[3] NUCLEOTIDE SEQUENCE OF 633-993.

STRAIN=Type B / NCTC 7273;

MEDLINE=94013372; PubMed=8408542 [NCBI, ExPASy, EBI, Israel, Japan]

Campbell K.D., Collins M.D., East A.K.;

"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";

J. Clin. Microbiol. 31:2255-2262(1993).

[4] PROTEIN SEQUENCE OF 1-44 AND 441-466.

STRAIN=Type B / B-657;

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# UniProtKB/Swiss-Prot entry P10844

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name BXB\_CLOBO

Primary accession number P10844
Secondary accession number P10843

Entered in Swiss-Prot in Release 11, July 1989
Sequence was last modified in Release 26, July 1993
Annotations were last modified in Release 47, May 2005

Name and origin of the protein

Protein name Botulinum neurotoxin type B [Precursor]

Synonyms EC 3.4.24.69
BoNT/B

Bontoxilysin B

Gene name Name: botB

From Clostridium botulinum [TaxID: 1491]

Taxonomy Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

Clostridium.

#### References

#### [1] NUCLEOTIDE SEQUENCE.

MEDLINE=92384550; PubMed=1514783 [NCBI, ExPASy, EBI, Israel, Japan]

Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T., Minton N.P.;

"Molecular cloning of the Clostridium botulinum structural gene encoding the type B neurotoxin and determination of its entire nucleotide sequence.";

Appl. Environ. Microbiol. 58:2345-2354(1992).

#### [2] NUCLEOTIDE SEQUENCE OF 35-245.

STRAIN=Type B / NCTC 7273;

Szabo E.A., Pemberton J.M., Desmarchelier P.M.;

Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

#### [3] NUCLEOTIDE SEQUENCE OF 633-993.

STRAIN=Type B / NCTC 7273;

MEDLINE=94013372; PubMed=8408542 [NCBI, ExPASy, EBI, Israel, Japan]

Campbell K.D., Collins M.D., East A.K.;

"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";

J. Clin. Microbiol. 31:2255-2262(1993).

PROTEIN SEQUENCE OF 1-44 AND 441-466. STRAIN=Type B / B-657;

DOI=10.1016/0300-9084(88)90111-3;MEDLINE=89000987;PubMed=3139097 [NCBI, ExPASy, EBI, Israel, Japan]

Dasgupta B.R., Datta A.;

"Botulinum neurotoxin type B (strain 657): partial sequence and similarity with tetanus toxin."; Biochimie 70:811-817(1988).

[5] PROTEIN SEQUENCE OF 1-16 AND 441-458.

**STRAIN**=Type B / Okra;

MEDLINE=85197963; PubMed=3888113 [NCBI, ExPASy, EBI, Israel, Japan]

Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;

"Partial amino acid sequences of botulinum neurotoxins types B and E.":

Arch. Biochem. Biophys. 238:544-548(1985).

[6] IDENTIFICATION AS ZINC-PROTEASE.

MEDLINE=93054694; PubMed=1429690 [NCBI, ExPASy, EBI, Israel, Japan]

Schiavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.;

"Botulinum neurotoxins are zinc proteins.";

J. Biol. Chem. 267:23479-23483(1992).

[7] IDENTIFICATION OF SUBSTRATE.

DOI=10.1038/359832a0;MEDLINE=93063293;PubMed=1331807 [NCBI, ExPASy, EBI, Israel, Japan]

Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucco C.; "Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin.";

Nature 359:832-835(1992).

#### Comments

- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that cleaves the 76-Gln-|-Phe-77 bond of synaptobrevin-2.
- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
- SUBCELLULAR LOCATION: Secreted.
- MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
- SIMILARITY: Belongs to the peptidase M27 family [view classification].

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#### Cross-references

	M81186; AAA23211.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
EMBL	Z11934; CAA77991.1; -;	[EMBL / GenBank / DDBJ]
ENIBL	Genomic_DNA.	[CoDingSequence]
	X70817; CAA50148.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]

DOI=10.1016/0300-9084(88)90111-3;MEDLINE=89000987;PubMed=3139097 [NCBI, ExPASy, EBI, Israel, Japan]

Dasgupta B.R., Datta A.:

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[5] PROTEIN SEQUENCE OF 1-16 AND 441-458.

STRAIN=Type B / Okra;

MEDLINE=85197963; PubMed=3888113 [NCBI, ExPASy, EBI, Israel, Japan]

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"Botulinum neurotoxins are zinc proteins.";

J. Biol. Chem. 267:23479-23483(1992).

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DOI=10.1038/359832a0;MEDLINE=93063293;PubMed=1331807 [NCBI, ExPASy, EBI, Israel, Japan]

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Nature 359:832-835(1992).

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	Genomic_DNA.	[CoDingSequence]
EMBL	Z11934; CAA77991.1; -;	[EMBL / GenBank / DDBJ]
LIVIBL	Genomic_DNA.	[CoDingSequence]
	X70817; CAA50148.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]

PIR A48940; A48940. 1EPW; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1F31; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1F82; X-ray; A=1-424. [ExPASy / RCSB / EBI] 1F83; X-ray; A=1-425. [ExPASy / RCSB / EBI] 1FQH; X-ray; A=1-424. [ExPASy / RCSB / EBI] 1G9A, X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1G9B; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1G9C; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1G9D; X-ray; A=1-1290. [ExPASy / RCSB / EBI] **PDB** 1I1E; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0B; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0C; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0D; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0E; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0F; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0G; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1Z0H; X-ray; A/B=-. [ExPASy / RCSB / EBI] Detailed list of linked structures. **MEROPS** M27.002; -. IPR011591; Botulinum. IPR006025; Pept M Zn BS. InterPro IPR000395; Peptidase M27. Graphical view of domain structure. PF01742; Peptidase M27; 1. Pfam Pfam graphical view of domain structure. **PRINTS** PR00760; BONTOXILYSIN. PD001963; Botulinum; 1. ProDom [Domain structure / List of seq. sharing at least 1 domain] **PROSITE** PS00142; ZINC PROTEASE; 1. HOGENOM [Family / Alignment / Tree] **BLOCKS** P10844. ProtoNet P10844. **ProtoMap** P10844. **PRESAGE** P10844. DIP P10844. ModBase P10844. SWISS-Get region on 2D PAGE. 2DPAGE UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.

#### Features



Feature table viewer



Feature aligner

PIR A48940; A48940. 1EPW, X-ray, A=1-1290 [ExPASy / RCSB / EBI] 1F31; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1F82; X-ray; A=1-424. [ExPASy / RCSB / EBI] 1F83; X-ray; A=1-425. [ExPASy / RCSB / EBI] 1FQH; X-ray; A=1-424. [ExPASy/RCSB/EBI] 1G9A, X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1G9B; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1G9C; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1G9D; X-ray; A=1-1290. [ExPASy / RCSB / EBI] **PDB** 111E; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0B; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0C; X-ray; A=1-1290 [ExPASy / RCSB / EBI] 1S0D; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0E; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0F; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1S0G; X-ray; A=1-1290. [ExPASy / RCSB / EBI] 1Z0H; X-ray; A/B=-. [ExPASy / RCSB / EBI] Detailed list of linked structures. **MEROPS** M27.002; -. IPR011591; Botulinum. IPR006025; Pept M Zn BS. InterPro IPR000395; Peptidase M27. Graphical view of domain structure. PF01742; Peptidase M27; 1. Pfam Pfam graphical view of domain structure. **PRINTS** PR00760; BONTOXILYSIN. PD001963; Botulinum; 1. ProDom [Domain structure / List of seq. sharing at least 1 domain] PROSITE PS00142; ZINC PROTEASE; 1. **HOGENOM** [Family / Alignment / Tree] **BLOCKS** P10844. **ProtoNet** P10844. ProtoMap P10844. **PRESAGE** P10844. DIP P10844. ModBase P10844. SWISS-Get region on 2D PAGE. 2DPAGE UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.

### Features



Feature table viewer



Feature aligner

Key INIT MET	From 0	<b>To</b> 0	Length	Description
CHAIN	1	440	440	Botulinum neurotoxin B light-chain.
CHAIN	441	1290	850	Botulinum neurotoxin B heavy-chain.
ACT SITE	230	230		By similarity.
METAL	229	229		Zinc (catalytic) (By similarity).
METAL	233	233		Zinc (catalytic) (By similarity).
DISULFID	436	445		Interchain (between light and heavy chains) (Probable).
CONFLICT	29	29		T -> M (in Ref. 4).
CONFLICT	217	217		R -> G (in Ref. 2).
CONFLICT	224	224		A -> S (in Ref. ?).
CONFLICT	463	463		$S \rightarrow R \text{ (in Ref. 4)}.$
TURN	9	10	2	
STRAND	18	22	5	
HELIX	24	26	3	
TURN	27	28	2	
STRAND	33	39	7	
TURN	40	41	2	
STRAND	42	45	4	
TURN	51	52	2	
HELIX	55	58	4	
STRAND	63	64	2	
TURN	67	68	2	
STRAND	71	73	3	
TURN	75	78	4	
HELIX	81	98	18	
TURN	99	100	2	
HELIX	102	113	12	
TURN	121	122	2	
TURN	125	126	2	
STRAND	127	128	2	
TURN	133	135	3	
STRAND	136	140	5	
TURN	144	145	2	
STRAND	150	154	5	
STRAND	157	160	4	
STRAND	165	165	1	
TURN	166	167	2	
STRAND	170	172	3	
STRAND	175	176	2	·
TURN	177	178	2	
STRAND	179	180	2	•
HELIX	181	183	3	
TURN	184	185	2	
STRAND	190	193	4	
STRAND	198	202	5	
TURN	205	206	2	

Key INIT_MET	From 0	<b>To</b> 0	Length	Description
CHAIN	1	440	440	Botulinum neurotoxin B light-chain.
CHAIN	441	1290	850	Botulinum neurotoxin B heavy-chain.
ACT_SITE	230	230		By similarity.
METAL	229	229		Zinc (catalytic) (By similarity).
METAL	233	233		Zinc (catalytic) (By similarity).
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CONFLICT	29	29		T -> M (in Ref. 4).
CONFLICT	217	217		R -> G (in Ref. 2).
CONFLICT	224	224		$A \rightarrow S \text{ (in Ref. 2)}.$
CONFLICT	463	463		$S \rightarrow R \text{ (in Ref. 4)}.$
TURN	9	10	2	
STRAND	18	22	5	·
HELIX	24	26	3	
TURN	27	28	2	
STRAND	33	39	7	
TURN	40	41	2	
STRAND	42	45	4	
TURN	51	52	2	
HELIX	55	58	4	
STRAND	63	64	2	
TURN	67	68	2	
STRAND	71	73	3	
TURN	75	78	4	
HELIX	81	98	18	•
TURN	99	100	2	
HELIX	102	113	12	
TURN	121	122	2	
TURN	125	126	2	
STRAND	127	128	2	
TURN	133	135	3	
STRAND	136	140	5	
TURN	144	145	2	
STRAND	150	154	5	
STRAND	157	160	4	
STRAND	165	165	1	
TURN	166	167	2	
STRAND	170	172	3	
STRAND	175	176	2	
TURN	177	178	2	
STRAND	179	180	2	
HELIX	181	183	3	
TURN	184	185	2	
STRAND	190	193	4	
STRAND	198	202	5	
TURN	205	206	2	

TURN	210	211	2
STRAND	219	220	2
HELIX	223	238	16
TURN	239	240	2
STRAND	248	248	1
STRAND	250	250	1
TURN	255	256	2
STRAND	257	257	1
STRAND	263	263	1
HELIX	265	271	7
TURN	273	274	2
HELIX	275	278	4
HELIX	281	304	24
STRAND	307	308	2
TURN	312	313	2
HELIX	316	326	11
TURN	327	328	2
STRAND	330	331	2
TURN	333	334	2
STRAND	337	338	2
HELIX	341	353	13
TURN	354	354	1
HELIX	357	364	8
TURN	365	365	1
STRAND	377	382	6
TURN	385	386	2
TURN	388	390	3
STRAND	392	392	1
TURN	393	395	3
STRAND	396	396	1
TURN	397	397	1
HELIX	400	402	3
TURN	403	403	1
HELIX	406	411	6
STRAND	412	412	1
TURN	413	415	3
HELIX	417	419	3
STRAND	420	421	2
HELIX	425	427	3
STRAND	428	429	2
STRAND	432	436	5
STRAND	445	449	5
HELIX	450	452	3
STRAND	454	454	1
STRAND	457	457	1
HELIX	459	461	3
HELIX	465	467	3
STRAND	470	472	3

TURN	210	211	2
STRAND	219	220	2
HELIX	223	238	16
TURN	239	240	2
STRAND	248	248	1
STRAND	250	250	1
TURN	255	256	2
STRAND	257	257	1
STRAND	263	263	1
HELIX	265	271	7
TURN	273	274	2
HELIX	275	278	4
HELIX	281	304	24
STRAND	307	308	2
TURN	312	313	2
HELIX	316	326	11
TURN	327	328	2
STRAND	330	331	2
TURN	333	334	2
STRAND	337	338	2
HELIX	341	353	13
TURN	354	354	1
HELIX	357	364	8
TURN	365	365	1
STRAND	377	382	6
TURN	385	386	2
TURN	388	390	3
STRAND	392	392	1
TURN	393	395	3
STRAND	396	396	1
TURN	397	397	1
HELIX	400	402	3
TURN	403	403	1
HELIX	406	411	6
STRAND	412	412	1
TURN	413	415	3
HELIX	417	419	3
STRAND	420	421	2
HELIX	425	427	3
STRAND	428	429	2
STRAND	432	436	5
STRAND	445	449	5
HELIX	450	452	3
STRAND	454	454	1
STRAND	457	457	1
HELIX	459	461	3
HELIX	465	467	3
STRAND	470	472	3

HELIX	487	492	6
STRAND	506	507	2
STRAND	516	516	1
STRAND	523	524	2
STRAND	526	530	5
HELIX	536	541	6
TURN	542	543	2
TURN	547	548	2
STRAND	553	555	3
HELIX	558	563	6
TURN	565	566	2
STRAND	567	569	3
HELIX	574	580	7
TURN	581 .	581	1
HELIX	586	605	20
HELIX	606	608	3
STRAND	611	611	1
HELIX	612	614	3
TURN	615	615	1
STRAND	616	616	1
TURN	621	622	2
HELIX	623	627	5
TURN	630	634	5
HELIX	638	645	8
HELIX	646	650	5
STRAND	665	667	3
TURN	671	672	2
HELIX	674	706	33
TURN	707	707	1
HELIX	708	737	30
TURN	738	739	2
HELIX	742	746	5
TURN	747	747	1
HELIX	752	785	34
TURN	786 ·	786	1
HELIX	787	811	25
TURN	812	812	1
HELIX	813	816	4
TURN	818	823	6
HELIX	824	830	7
TURN	831	832	2
HELIX	839	841	3
TURN	842	842	1
HELIX	846	856	11
TURN	857	857	1
HELIX	859	862	4
STRAND	863	869	7
STRAND	874	876	3

HELIX	487	492	6
STRAND	506	507	2
STRAND	516	516	1
STRAND	523	524	2
STRAND	526	530	5
HELIX	536	541	6
TURN	542	543	2
TURN	547	548	2
STRAND	553	555	3
HELIX	558	563	6
TURN	565	566	2
STRAND	567	569	3
HELIX	574	580	7
TURN	581	581	1
HELIX	586	605	20
HELIX	606	608	3
STRAND	611	611	1
HELIX	612	614	3
TURN	615	615	1
STRAND	616	616	1
TURN	621	622	2
HELIX	623	627	5
TURN	630	634	5
HELIX	638	645	8
HELIX	646	650	5
STRAND	665	667	3
TURN	671	672	2
HELIX	674	706	33
TURN	707	707	1
HELIX	708	737	30
TURN	738	739	2
HELIX	742	746	5
TURN	747	747	1
HELIX	752	785	34
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HELIX	787	811	25
TURN	812	812	1
HELIX	813	816	4
TURN	818	823	6
HELIX	824	830	7
TURN	831	832	2
HELIX	839	841	3
TURN	842	842	1
HELIX	846	856	11
TURN	857	857	1
HELIX	859	862	4
STRAND	863	869	7
STRAND	874	876	3

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STRAND	883	886	4
TURN	888	889	2
STRAND	891	892	2
TURN	894	895	2
STRAND	897	900	4
TURN	904	905	2
STRAND	908	911	4
TURN	914	915	2
STRAND	925	932	8
HELIX	938	940	, 3
HELIX	941	946	6
STRAND	948	956 .	9
TURN	957	958	2
STRAND	959	966	8
TURN	967	968	2
STRAND	969	975	7
TURN	977	978	2
STRAND	981	987	7
TURN	998	999	2
STRAND	1002	1008	7
STRAND	1012	1017	6
TURN	1018 .	1019	2
STRAND	1020	1026	7
STRAND	1038	1045	8
TURN	1049	1050	2
STRAND	1053	1061	9
HELIX	1067	1078	12
STRAND	1082	1082	1
STRAND	1084	1084	1
TURN	1086	1087	2
STRAND	1090	1090	1
STRAND	1092	1093	2
TURN	1094	1094	1
STRAND	1096	1101	6
TURN	1102	1103	2
TURN	1105	1106	2
STRAND	1107	1111	5
TURN	1113	1114	2
STRAND	1118	1122	5
STRAND	1125	1125	1
STRAND	1136	1136	1
STRAND	1144	1148	5
STRAND	1158	1159	2
STRAND	1161	1161	1
TURN	1162	1163	2
STRAND	1165	1172	8
TURN	1173	1174	2
STRAND	1175	1182 ′	8

STRAND	883	886	4
TURN	888	889	2
STRAND	891	892	2
TURN	894	895	2
STRAND	897	900	4
TURN	904	905	2
STRAND	908	911	4
TURN	914	915	2
STRAND	925	932	8
HELIX	938	940	3
HELIX	941	946	6
STRAND	948	956	9
TURN	957	958	2
STRAND	959	966	8
TURN	967	968	2
STRAND	969	975	7
TURN	977	978	2
STRAND	981	987	7
TURN	998	999	2
STRAND	1002	1008	7
STRAND	1012	1017	6
TURN	1018	1019	2
STRAND	1020	1026	7
STRAND	1038	1045	8
TURN	1049	1050	2
STRAND	1053	1061	9
HELIX	1067	1078	12
STRAND	1082	1082	1
STRAND	1084	1084	1
TURN	1086	1087	2
STRAND	1090	1090	1
STRAND	1092	1093	2
TURN	1094	1094	. 1
STRAND	1096	1101	6
TURN	1102	1103	2
TURN	1105	1106	2
STRAND	1107	1111	5
TURN	1113	1114	2
STRAND	1118	1122	5
STRAND	1125	1125	1
STRAND	1136	1136	1
STRAND	1144	1148	5
STRAND	1158	1159	2
STRAND	1161	1161	1
TURN	1162	1163	2
STRAND	1165	1172	8
TURN	1173	1174	2
STRAND	1175	1182	8

TURN.	1183	1184	2
STRAND	1189	1191	3
STRAND	1193	1196	4
TURN	1201	1202	2
STRAND	1203	1204	2
STRAND	1207	1210	4
STRAND	1220	1225	6
STRAND	1233	1245	13
STRAND	1250	1259	10
TURN	1260	1260	1
HELIX	1261	1265	5
TURN	1266	1267	2
TURN	1273	1274	2
TURN	1276	1277	2
STRAND	1279	1282	4
STRAND	1285	1285	1
TURN	1286	1287	2
STRAND	1288	1288	1

# Sequence information Length: 1200 AA [This is the

length of the	AA [This is tunprocessed	[This is the	ne MW of the	C.	RC64: <b>D21746E2C024DF43</b> [This a checksum on the sequence]
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PVTINNFNYN	DPIDNNNIIM	MEPPFARGTG	RYYKAFKITD	RIWIIPERYT	FGYKPEDFNK
7 <u>0</u> SSGIFNRDVC	8 <u>0</u> EYYDPDYLNT		10 <u>0</u> MIKLFNRIKS		12 <u>0</u> IINGIPYLGD
	14 <u>0</u>	15 <u>0</u>	16 <u>0</u>	17 <u>0</u>	18 <u>0</u>
	NIASVTVNKL	ISNPGEVERK	KGIFANLIIF	GPGPVLNENE	TIDIGIQNHF
	20 <u>0</u> QMKFCPEYVS			23 <u>0</u> SDPALILMHE	
25 <u>0</u>	26 <u>0</u>	27 <u>0</u>	28 <u>0</u>	29 <u>0</u>	30 <u>0</u>
IKVDDLPIVP	NEKKFFMQST	DAIQAEELYT	FGGQDPSIIT	PSTDKSIYDK	VLQNFRGIVD
31 <u>0</u> RLNKVLVCIS	32 <u>0</u> DPNININIYK				36 <u>0</u> LMFGFTETNI
37 <u>0</u>	38 <u>0</u>	39 <u>0</u>	40 <u>0</u>	41 <u>0</u>	42 <u>0</u>
AENYKIKTRA	SYFSDSLPPV	KIKNLLDNEI	YTIEEGFNIS	DKDMEKEYRG	QNKAINKQAY
43 <u>0</u>	44 <u>0</u>	45 <u>0</u>	46 <u>0</u>	47 <u>0</u>	48 <u>0</u>
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49 <u>0</u>	50 <u>0</u>	51 <u>0</u>	52 <u>0</u>	53 <u>0</u>	54 <u>0</u>
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55 <u>0</u>	56 <u>0</u>	57 <u>0</u>	58 <u>0</u>	59 <u>0</u>	60 <u>0</u>
YSQTFPLDIR	DISLTSSFDD	ALLFSNKVYS	FFSMDYIKTA	NKVVEAGLFA	GWVKQIVNDF
61 <u>0</u> VIEANKSNTM	62 <u>0</u> DKIADISLIV	63 <u>0</u> PYIGLALNVG			

TURN	1183	1184	2
STRAND	1189	1191	3
STRAND	1193	1196	4
TURN	1201	1202	2
STRAND	1203	1204	2
STRAND	1207	1210	4
STRAND	1220	1225	6
STRAND	1233	1245	13
STRAND	1250	1259	10
TURN	1260	1260	1
HELIX	1261	1265	5
TURN	1266	1267	2
TURN	1273	1274	2
TURN	1276	1277	2
STRAND	1279	1282	4
STRAND	1285	1285	1
TURN	1286	1287	2
STRAND	1288	1288	1

### Sequence information

Length: 1290 length of the precursor]	AA [This is tunprocessed	[This is the			CRC64: <b>D21746E2C024DF43</b> [This is a checksum on the sequence]		
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		15 <u>0</u> ISNPGEVERK					
19 <u>0</u> ASREGFGGIM	20 <u>0</u> QMKFCPEYVS	21 <u>0</u> VFNNVQENKG	22 <u>0</u> ASIFNRRGYF	23 <u>0</u> SDPALILMHE	24 <u>0</u> LIHVLHGLYG		
		27 <u>0</u> DAIQAEELYT			30 <u>0</u> VLQNFRGIVD		
		33 <u>0</u> NKFKDKYKFV			36 <u>0</u> LMFGFTETNI		
37 <u>0</u> AENYKIKTRA	38 <u>0</u> SYFSDSLPPV	39 <u>0</u> KIKNLLDNEI	40 <u>0</u> YTIEEGFNIS	41 <u>0</u> DKDMEKEYRG	42 <u>0</u> QNKAINKQAY		
43 <u>0</u> EEISKEHLAV	44 <u>0</u> YKIQMCKSVK	45 <u>0</u> APGICIDVDN	46 <u>0</u> EDLFFIADKN	47 <u>0</u> SFSDDLSKNE	48 <u>0</u> RIEYNTQSNY		
49 <u>0</u> IENDFPINEL		51 <u>0</u> ELPSENTESL	52 <u>0</u> TDFNVDVPVY	53 <u>0</u> EKQPAIKKIF			
55 <u>0</u> YSQTFPLDIR		57 <u>0</u> ALLFSNKVYS	58 <u>0</u> FFSMDYIKTA	59 <u>0</u> NKVVEAGLFA			
61 <u>0</u> VIEANKSNTM		63 <u>0</u> PYIGLALNVG		65 <u>0</u> AFEIAGASIL			

67 <u>0</u> VVGAFLLESY	68 <u>0</u> IDNKNKIIKT	69 <u>0</u> IDNALTKRNE	70 <u>0</u> KWSDMYGLIV	71 <u>0</u> AQWLSTVNTQ	72 <u>0</u> FYTIKEGMYK	
73 <u>0</u> ALNYQAQALE	74 <u>0</u> EIIKYRYNIY	75 <u>0</u> SEKEKSNINI	76 <u>0</u> DFNDINSKLN	77 <u>0</u> EGINQAIDNI	78 <u>0</u> NNFINGCSVS	
79 <u>0</u> YLMKKMI PLA	80 <u>0</u> VEKLLDFDNT	81 <u>0</u> LKKNLLNYID				
	86 <u>0</u> MFNKYNSEIL					
	92 <u>0</u> TQNQNIIFNS					
97 <u>0</u> WKISIRGNRI	98 <u>0</u> IWTLIDINGK	99 <u>0</u> TKSVFFEYNI	100 <u>0</u> REDISEYINR	101 <u>0</u> WFFVTITNNL	102 <u>0</u> NNAKIYINGK	
103 <u>0</u> LESNTDIKDI	104 <u>0</u> REVIANGEII	105 <u>0</u> FKLDGDIDRT	106 <u>0</u> QFIWMKYFSI	107 <u>0</u> FNTELSQSNI	108 <u>0</u> EERYKIQSYS	
	110 <u>0</u> LMYNKEYYMF					
115 <u>0</u> GEKFIIRRKS	116 <u>0</u> NSQSINDDIV	117 <u>0</u> RKEDYIYLDF	118 <u>0</u> FNLNQEWRVY	119 <u>0</u> TYKYFKKEEE	120 <u>0</u> KLFLAPISDS	
	122 <u>0</u> EYDEQPTYSC					
	128 <u>0</u> YNLKLGCNWQ					P10844 in FASTA format

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	68 <u>0</u> IDNKNKIIKT				
73 <u>0</u> ALNYQAQALE	74 <u>0</u> EIIKYRYNIY	75 <u>0</u> SEKEKSNINI			
	80 <u>0</u> VEKLLDFDNT				
	86 <u>0</u> MFNKYNSEIL				
	92 <u>0</u> TQNQNIIFNS				
	98 <u>0</u> IWTLIDINGK				
	104 <u>0</u> REVIANGEII				
	110 <u>0</u> LMYNKEYYMF	111 <u>0</u> NAGNKNSYIK			
	116 <u>0</u> NSQSINDDIV				
	122 <u>0</u> EYDEQPTYSC				
	128 <u>0</u> YNLKLGCNWQ		•	·	P10844 in FASTA format

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Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the <u>online BLAST help</u>.

If your question is not covered, please contact <<u>helpdesk@expasy.org</u>>.

NCBI BLAST program reference [PMID: 9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 465 AA (of which 5% low-complexity regions filtered out)

Date run: 2005-05-12 15:03:56 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,906,987 sequences; 613,355,151 total letters

UniProt Release 5.0 consists of: Swiss-Prot Release 47.0 of 10-May-2005: 181571 en

TrEMBL Release 30.0 of 10-May-2005: 1714475 entrie

Taxonomic view NiceBlast view Printable view

#### List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment)

Select up to

Submit Query

#### Include query sequence

	Db AC	Description	core E-	value
	sp <u>F10844</u>	BXB_CLOBO Botulinum neurotoxin type B precursor (EC 3	<u>905</u>	0.0
	tr <u>Q93G71</u>	_CLOBO Neurotoxin type B [Clostridium botulinum]	<u>853</u>	0.0
	tr <u>Q933K0</u>	_CLOBO Type B cryptic neurotoxin [Clostridium botulinum]	852	0.0
	tr <u>Q</u> 9ZAJ8	_CLOBO BonT protein [bonT] [Clostridium botulinum]	850	0.0
	tr <u>Q8GR96</u>	_CLOBO Neurotoxin [bontb] [Clostridium botulinum]	831	0.0
	tr <u>008077</u>	_CLOBO BoNT/B [bont/b] [Clostridium botulinum]	800	0.0
Γ	tr <u>Q9X708</u>	_CLOBO Botulinum neurotoxin type B (Fragment) [boNT/B]	. <u>791</u>	0.0
	sp <u>Q60393</u>	BXG_CLOBO Botulinum neurotoxin type G precursor (EC 3	468 e	-130
	sp <u>P10845</u>	BXA1_CLOBO Botulinum neurotoxin type A precursor (EC 3	<u>316</u> 6	5e-85
$\Box$	tr <u>Q7B8V4</u>	_CLOBO BoNT/A [bont/a] [Clostridium botulinum]	<u>316</u> 6	5e-85

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If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the online BLAST help. If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]: Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 465 AA (of which 5% low-complexity regions filtered out)

Date run: 2005-05-12 15:03:56 UTC+0100 on sib-gml.unil.ch

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TrEMBL Release 30.0 of 10-May-2005: 1714475 entrie

Taxonomic view NiceBlast view Printable view

#### List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to ..

#### Include query sequence

	Db AC	Description S	core E-	value
П	sp <u>P10844</u>	BXB_CLOBO Botulinum neurotoxin type B precursor (EC 3	<u>905</u>	0.0
	tr <u>Q93G71</u>	_CLOBO Neurotoxin type B [Clostridium botulinum]	<u>853</u>	0.0
	tr <u>Q933K0</u>	_CLOBO Type B cryptic neurotoxin [Clostridium botulinum]	852	0.0
	tr <u>Q9ZAJ8</u>	_CLOBO BonT protein [bonT] [Clostridium botulinum]	<u>850</u>	0.0
$\Box$	tr <u>Q8GR96</u>	_CLOBO Neurotoxin [bontb] [Clostridium botulinum]	<u>831</u>	0.0
	tr <u>Q08077</u>	_CLOBO BoNT/B [bont/b] [Clostridium botulinum]	800	0.0
	tr <u>Q9X708</u>	_CLOBO Botulinum neurotoxin type B (Fragment) [boNT/B]	. <u>791</u>	0.0
	sp <u>Q60393</u>	BXG_CLOBO Botulinum neurotoxin type G precursor (EC 3	<u>468</u> e	-130
	sp <u>P10845</u>	BXA1_CLOBO Botulinum neurotoxin type A precursor (EC 3	<u>316</u> 6	Se-85
	tr Q7B8V4	CLOBO BoNT/A [bont/a] [Clostridium botulinum]	316 6	Se-85

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\blacksquare tr <u>Q45851</u> 9CLOT Neurotoxin type F [bont /f] [Clostridium baratii]
                                                                                                                     301 2e-80
\blacksquare tr <u>Q45846</u> CLOBO Botulinum neurotoxin type B (Fragment) [BoNT/B] \dots <u>299</u> 1e-79
T tr <u>Q45848</u> CLOBO Botulinum neurotoxin type B (Fragment) [BoNT/B] ... <u>298</u> 2e-79
sp Q45894 BXA2 CLOBO Botulinum neurotoxin type A precursor (EC 3... 297 3e-79
T tr Q58GH1 CLOBO Type A2 botulinum neurotoxin [Clostridium botuli... 297 3e-79
tr Q9ZAJ5 CLOBO BonT protein [bonT] [Clostridium botulinum]
                                                                                                                     281 2e-74
tr <u>Q57236</u> _CLOBO BoNT/F (Neurotoxin type F) [bont/f] [Clostridium... <u>281</u> 3e-74
\square sp \underline{	ext{P30996}} BXF CLOBO Botulinum neurotoxin type F precursor (EC 3.... \underline{	ext{278}} 1e-73
\square sp <u>Q00496</u> BXE CLOBO Botulinum neurotoxin type E precursor (EC 3.... <u>273</u> 4e-72
tr Q9K395 CLOBU Type E botulinum toxin [bont/E] [Clostridium but... 267 3e-70
🗔 sp <u>P30995</u> BXE CLOBU Botulinum neurotoxin type E precursor (EC 3.... <u>266</u> 7e-70
🗔 tr Q9FAR6 CLOBU Type E botulinum toxin [bont/E] [Clostridium but... 266 9e-70
\square tr Q8KZM3 CLOBU Type E botulinum toxin [bont/E] [Clostridium but... 266 9e-70
sp <u>P19321</u> BXD CLOBO Botulinum neurotoxin type D precursor (EC 3.... 233 7e-60
tr Q9QTG7 CBDP NTX (Fragment) [ntx] [Clostridium botulinum D bac... 231 2e-59
🗔 tr <u>Q5DW55</u> CLOBO Type C botulinaum neurotoxin [bont/C] [Clostridi... 230 6e-59
tr <u>Q9LBS7</u> _CLOBO Type C botulinaum neurotoxin [bont/C] [Clostridi... <u>228</u> 3e-58
tr Q45849 CLOBO Neurotoxin [Clostridium botulinum C]
                                                                                                                     228 3e-58
tr <u>Q841S3</u> <u>CLOBO Neurotoxin</u> [Clostridium botulinum]
                                                                                                                     226 6e-58
sp P04958 TETX_CLOTE Tetanus toxin precursor (EC 3.4.24.68) (Ten... 211 2e-53
tr Q9LA13 CLOTE Tetanus toxin (Fragment) [Clostridium tetani]
                                                                                                                     211 4e-53
tr Q459<u>67</u> _CLOBO Neurotoxin consisting of botulinum neurotoxin D ... <u>206</u> 1e-51
tr <u>Q9LBR1</u> CLOBO Neurotoxin [Clostridium botulinum]
                                                                                                                     205 1e-51
tr <u>Q93N27</u> _CLOTE Tetanus toxin (Fragment) [Clostridium tetani]
                                                                                                                     200 5e-50
□ sp P18640 BXC1 CLOBO Botulinum neurotoxin type C1 precursor (EC ... 198 2e-49
tr Q93HT3 CLOBO Type C botulinaum neurotoxin [bont/C] [Clostridi... 198 2e-49
tr <u>Q7WUH9</u> _CLOBO Botulinum neurotoxin type B (Fragment) [bont/B] ... <u>148</u> 2e-34
tr <u>Q7WRW0</u> _CLOBO Botulinum neurotoxin type B (Fragment) [bont/B] ... <u>147</u> 6e-34
The tright of the tright of the contraction of the tright of tright of the tright of tright of the tright of tright
Tr Q79AH9 CLOBO Botulinum neurotoxin type F (Fragment) [BoNT/F] ... 142 1e-32
\square tr <u>Q45861</u> CLOBO Botulinum neurotoxin type E (Fragment) [BoNT/E] ... 133 7e-30
tr 006018 CLOBO NTNH protein [NTNH] [Clostridium botulinum]
                                                                                                                       86 2e-15
\square tr <u>Q45888</u> CLOBO Nontoxic-hemagglutinin [nontoxic-hemagglutinin] ... 77 6e-13
sp P46082 BXEN CLOBO Botulinum neurotoxin type E, nontoxic compo...
                                                                                                                       75 4e-12
tr Q9LBS8 CLOBO NTNHA [ntnha] [Clostridium botulinum]
                                                                                                                       75 4e-12
sp <u>Q06366</u> BXEN_CLOBU Botulinum neurotoxin type E, nontoxic compo...
                                                                                                                       74 5e-12
tr Q9ZAJ9 CLOBO Ntnh protein [ntnh] [Clostridium botulinum]
                                                                                                                       74 5e-12
tr P71117 CLOBO Nontoxic-nonhemagglutinin [nontoxic-nonhemagglut...
                                                                                                                     74 5e-12
tr <u>087710</u> _9CLOT NTNH protein [ntnh] [Clostridium baratii]
                                                                                                                       74 5e-12
tr <u>069277</u> _CLOBO Nontoxic-nonhaemagglutinin [ntnh] [Clostridium b... <u>74</u> 5e-12
tr 033871 _CLOBO Nontoxic-nonhemagglutinin component [ntnh/B] [Cl...
                                                                                                                      <u>74</u> 5e-12
tr <u>Q45893</u> CLOBO NTNH protein [ntnh] [Clostridium botulinum]
                                                                                                                       74 7e-12
tr Q9LBR2 _CLOBO NTNHA [ntnha] [Clostridium botulinum]
                                                                                                                       74 9e-12
\square sp <u>P46081</u> BXCN CLOBO Botulinum neurotoxin type C1, nontoxic comp...
                                                                                                                      72 3e-11
tr Q93HT4 _CLOBO NTNHA [ntnha] [Clostridium botulinum]
                                                                                                                       72 3e-11
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tr <u>Q45851</u> 9CLOT Neurotoxin type F [bont /f] [Clostridium baratii]
tr <u>Q45846</u> CLOBO Botulinum neurotoxin type B (Fragment) [BoNT/B] ... <u>299</u> 1e-79
Tr Q45848 CLOBO Botulinum neurotoxin type B (Fragment) [BoNT/B] ... 298 2e-79
sp Q45894 BXA2 CLOBO Botulinum neurotoxin type A precursor (EC 3... 297 3e-79
tr Q58GH1 CLOBO Type A2 botulinum neurotoxin [Clostridium botuli... 297 3e-79
tr Q9ZAJ5 CLOBO BonT protein [bonT] [Clostridium botulinum]
                                                                          281 2e-74
tr <u>Q57236</u> _CLOBO BoNT/F (Neurotoxin type F) [bont/f] [Clostridium... <u>281</u> 3e-74
sp <u>P30996</u> BXF CLOBO Botulinum neurotoxin type F precursor (EC 3.... <u>278</u> 1e-73
sp Q00496 BXE CLOBO Botulinum neurotoxin type E precursor (EC 3.... 273 4e-72
tr <u>Q9K395</u> CLOBU Type E botulinum toxin [bont/E] [Clostridium but... <u>267</u> 3e-70
sp P30995 BXE CLOBU Botulinum neurotoxin type E precursor (EC 3.... 266 7e-70
tr Q9FAR6 CLOBU Type E botulinum toxin [bont/E] [Clostridium but... 266 9e-70
tr Q8KZM3 _CLOBU Type E botulinum toxin [bont/E] [Clostridium but... 266 9e-70
sp P19321 BXD CLOBO Botulinum neurotoxin type D precursor (EC 3.... 233 7e-60
tr Q9QTG7 CBDP NTX (Fragment) [ntx] [Clostridium botulinum D bac... 231 2e-59
tr Q5DW55 CLOBO Type C botulinaum neurotoxin [bont/C] [Clostridi... 230 6e-59
tr Q9LBS7 CLOBO Type C botulinaum neurotoxin [bont/C] [Clostridi... 228 3e-58
tr Q45849 CLOBO Neurotoxin [Clostridium botulinum C]
                                                                          228 3e-58
tr Q841S3 CLOBO Neurotoxin [Clostridium botulinum]
                                                                          226 6e-58
sp P04958 TETX CLOTE Tetanus toxin precursor (EC 3.4.24.68) (Ten...
                                                                          211 2e-53
tr Q9LA13 CLOTE Tetanus toxin (Fragment) [Clostridium tetani]
                                                                          211 4e-53
\square tr <u>Q45967</u> CLOBO Neurotoxin consisting of botulinum neurotoxin D ... <u>206</u> 1e-51
tr Q9LBR1 CLOBO Neurotoxin [Clostridium botulinum]
                                                                          205 1e-51
tr Q93N27 CLOTE Tetanus toxin (Fragment) [Clostridium tetani]
                                                                          200 5e-50
sp P18640 BXC1 CLOBO Botulinum neurotoxin type C1 precursor (EC ... 198 2e-49
T tr Q93HT3 CLOBO Type C botulinaum neurotoxin [bont/C] [Clostridi... 198 2e-49
tr <u>Q7WUH9</u> CLOBO Botulinum neurotoxin type B (Fragment) [bont/B] ... <u>148</u> 2e-34
tr Q7WRW0 CLOBO Botulinum neurotoxin type B (Fragment) [bont/B] ... 147 6e-34
\square tr <u>Q6Q799</u> CLOBO Non-proteolytic neurotoxin type B (Fragment) {Cl... <u>146</u> 1e-33
\square tr <u>Q79AH9</u> CLOBO Botulinum neurotoxin type F (Fragment) [BoNT/F] ... <u>142</u> 1e-32
\square tr <u>Q45861</u> CLOBO Botulinum neurotoxin type E (Fragment) [BoNT/E] ... <u>133</u> 7e-30
tr 006018 CLOBO NTNH protein [NTNH] [Clostridium botulinum]
                                                                           86 2e-15
\blacksquare tr <u>Q45888</u> CLOBO Nontoxic-hemagglutinin [nontoxic-hemagglutinin] ... 77 6e-13
sp P46082 BXEN CLOBO Botulinum neurotoxin type E, nontoxic compo...
                                                                           <u>75</u> 4e-12
tr Q9LBS8 CLOBO NTNHA [ntnha] [Clostridium botulinum]
                                                                           75 4e-12
sp Q06366 BXEN CLOBU Botulinum neurotoxin type E, nontoxic compo...
                                                                           74 5e-12
tr Q9ZAJ9 CLOBO Ntnh protein [ntnh] [Clostridium botulinum]
                                                                           <u>74</u> 5e-12
tr <u>P71117</u> _CLOBO Nontoxic-nonhemagglutinin [nontoxic-nonhemagglut...
                                                                          74 5e-12
tr 087710 9CLOT NTNH protein [ntnh] [Clostridium baratii]
                                                                           74 5e-12
\square tr <u>069277</u> CLOBO Nontoxic-nonhaemagglutinin [ntnh] [Clostridium b...
                                                                           74 5e-12
tr 033871 _CLOBO Nontoxic-nonhemagglutinin component [ntnh/B] [Cl...
                                                                           74 5e-12
tr <u>Q45893</u> <u>CLOBO NTNH protein [ntnh] [Clostridium botulinum]</u>
                                                                           74 7e-12
tr Q9LBR2 CLOBO NTNHA [ntnha] [Clostridium botulinum]
                                                                           74 9e-12
sp <u>P46081</u> BXCN_CLOBO Botulinum neurotoxin type C1, nontoxic comp...
                                                                           <u>72</u> 3e-11
tr Q93HT4 _CLOBO NTNHA [ntnha] [Clostridium botulinum]
                                                                           72 3e-11
```

```
tr Q45916 CLOBO 138kDa protein associated with BoNT /Cl-haemaggl...
                                                                          72 3e-11
tr Q9ZX77 _CBDP NTNH [ntnh] [Clostridium botulinum D bacteriophage]
                                                                          72 3e-11
tr Q38197 _9VIRU ANTP-139 protein [ANTP-139] [Clostridium botulin...
                                                                          72 3e-11
tr <u>Q53550</u> CLOBO Progenitor toxin L nontoxic-nonhemagglutinin com...
                                                                          72 3e-11
tr <u>Q45891</u> CLOBO NTNH protein [ntnh] [Clostridium botulinum]
                                                                          71 6e-11
tr Q45880 CLOBO NtnhA protein [ntnhA] [Clostridium botulinum]
                                                                          69 2e-10
tr 069276 CLOBO Nontoxic-nonhaemagglutinin [ntnh] [Clostridium b...
                                                                          <u>69</u> 2e-10
T tr Q45887 CLOBO Botulinum neurotoxin type F nontoxic-nonhemaglut...
                                                                          68 5e-10
tr Q45844 CLOBO Neurotoxin complex M nontoxic-nonhemagglutinin c...
                                                                          68 5e-10
tr Q564H3 9CLOT Neurotoxin heavy chain [Clostridium sp. RKD]
                                                                          64 9e-09
tr <u>Q9ZAJ6</u> _CLOBO Ntnh protein [ntnh] [Clostridium botulinum]
                                                                          64 9e-09
\blacksquare tr <u>Q45914</u> CLOBO Type A progenitor toxin nontoxic-nonHA (NTNH) [a...
                                                                          63 1e-08
tr P71107 _CLOBO Ntnh protein [ntnh] [Clostridium botulinum A]
                                                                          63 1e-08
tr <u>Q45850</u> _CLOBO Ntnh protein [ntnh] [Clostridium botulinum]
                                                                          63 2e-08
tr <u>P71108</u> CLOBO Nontoxic-nonhemagglutinin component [Clostridium...
                                                                         62 3e-08
tr P71109 _CLOBO Nontoxic-nonhemagglutinin [ntnh] [Clostridium bo...
                                                                          61 5e-08
tr <u>Q7WUH7</u> CLOBU Botulinum neurotoxin type E (Fragment) [bont/E] ...
                                                                          49 2e-04
tr Q8ILA2 PLAF7 Hypothetical protein [PF14 0343] [Plasmodium fal...
                                                                          48 4e-04
tr Q8IBF4 PLAF7 Hypothetical protein MAL7P1.167 [MAL7P1.167] [Pl...
                                                                          48 5e-04
tr Q7WRP2 _CLOBU Botulinum neurotoxin type E (Fragment) [bont/E] ...
                                                                          45 0.003
tr <u>Q6DN58</u> _KLULA COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (...
                                                                          45 0.004
tr <u>Q815X3</u> _PLAF7 Hypothetical protein [PFL0360c] [Plasmodium falc...
                                                                          44 0.008
tr <u>Q7RP92</u> _PLAYO Clp [PY01567] [Plasmodium yoelii yoelii]
                                                                          44 0.010
\square tr <u>Q7RDL0</u> _PLAYO Hypothetical protein [PY05412] [Plasmodium yoeli...
                                                                          44 0.010
tr Q6LFF0 PLAF7 Hypothetical protein [PFF0575c] [Plasmodium falc...
                                                                         44 0.010
tr Q8IDG1 _PLAF7 Hypothetical protein PF13_0283 [PF13_0283] [Plas...
                                                                          43 0.013
tr Q813X5 _PLAF7 Hypothetical protein PFE0655w [PFE0655w] [Plasmo...
                                                                          43 0.013
tr Q7RJM7 PLAYO Hypothetical protein [PY03232] [Plasmodium yoeli...
                                                                          43 0.013
tr Q9EMF0 _AMEPV AMV256 [AMV256] [Amsacta moorei entomopoxvirus (...
                                                                          42 0.022
tr Q8IIK5 PLAF7 Hypothetical protein [PF11_0168] [Plasmodium fal...
                                                                          42 0.029
tr Q7RB20 _PLAYO Hypothetical protein [PY06328] [Plasmodium yoeli...
                                                                          42 0.029
tr <u>Q8T186</u> DICDI Hypothetical protein [Dictyostelium discoideum (...
                                                                         42 0.037
tr <u>Q7RTC2</u> PLAYO Hypothetical protein (Fragment) [PY00072] [Plasm...
                                                                         42 0.037
tr <u>Q7RFF5</u> PLAYO Arabinogalactan protein [PY04751] [Plasmodium yo...
                                                                         41 0.064
tr Q8ILN7 _PLAF7 Hypothetical protein [PF14_0206] [Plasmodium fal...
                                                                         40 0.083
tr Q81462 _PLAF7 Hypothetical protein PFE0190c [PFE0190c] [Plasmo...
                                                                         40 0.083
tr <u>Q7RRG0</u> PLAYO Protein kinase domain, putative [PY00761] [Plasm...
                                                                         40 0.083
tr Q7RPW6 PLAYO Hypothetical protein (Fragment) [PY01338] [Plasm...
                                                                         40 0.083
sp P21358 RMAR_CANGA Mitochondrial ribosomal protein VAR1 [VAR1]...
                                                                          40 0.11
tr <u>Q8II48</u> _PLAF7 Hypothetical protein [PF11_0326] [Plasmodium fal...
                                                                          40 0.11.
tr <u>Q812R1</u> _PLAF7 Hypothetical protein PFI1210w [PFI1210w] [Plasmo...
                                                                          40 0.11
tr <u>Q7RQ77</u> _PLAYO Hypothetical protein [PY01225] [Plasmodium yoeli...
                                                                          40 0.11
tr Q6LFH3 _PLAF7 Hypothetical protein [PFF0460w] [Plasmodium falc...
                                                                          40 0.14
sp Q98PH2 MTLD_MYCPU Mannitol-1-phosphate 5-dehydrogenase (EC 1....
                                                                          <u>39</u> 0.19
tr Q8ID18 _PLAF7 Hypothetical protein MAL13P1.349 [MAL13P1.349] [...
                                                                         39 0.19
```

	tr <u>Q45916</u> CLOBO	138kDa protein associated with BoNT /C1-haemaggl	72	3e-11
		VTNH [ntnh] [Clostridium botulinum D bacteriophage]		3e-11
	tr <u>Q38197</u> _9VIRU	ANTP-139 protein [ANTP-139] [Clostridium botulin	72	3e-11
	tr <u>Q53550</u> _CLOBO	Progenitor toxin L nontoxic-nonhemagglutinin com	72	3e-11
	tr <u>Q45891</u> _CLOBO	NTNH protein [ntnh] [Clostridium botulinum]	71	6e-11
	tr <u>Q45880</u> _CLOBO	NtnhA protein [ntnhA] [Clostridium botulinum]	<u>69</u>	2e-10
	tr <u>069276</u> _CLOBO	Nontoxic-nonhaemagglutinin [ntnh] [Clostridium b	69	2e-10
	tr <u>Q45887</u> _CLOBO	Botulinum neurotoxin type F nontoxic-nonhemaglut	<u>68</u>	5e-10
	tr <u>Q45844</u> _CLOBO	Neurotoxin complex M nontoxic-nonhemagglutinin c	68	5e-10
	tr <u>Q564H3</u> _9CLOT	Neurotoxin heavy chain [Clostridium sp. RKD]	64	9e-09
	tr <u>Q9ZAJ6</u> _CLOBO	Ntnh protein [ntnh] [Clostridium botulinum]	64	9e-09
	tr <u>Q45914</u> _CLOBO	Type A progenitor toxin nontoxic-nonHA (NTNH) [a	63	1e-08
	tr <u>P71107</u> _CLOBO	Ntnh protein [ntnh] [Clostridium botulinum A]	<u>63</u>	1e-08
	tr <u>Q45850</u> _CLOBO	Ntnh protein [ntnh] [Clostridium botulinum]	63	2e-08
	tr <u>P71108</u> _CLOBO	Nontoxic-nonhemagglutinin component [Clostridium	<u>62</u>	3e-08
	tr <u>P71109</u> _CLOBO	Nontoxic-nonhemagglutinin [ntnh] [Clostridium bo	61	5e-08
	tr <u>Q7WUH7</u> _CLOBU	Botulinum neurotoxin type E (Fragment) [bont/E]	49	2e-04
	tr <u>Q8ILA2</u> _PLAF7	Hypothetical protein [PF14_0343] [Plasmodium fal	48	4e-04
	tr <u>Q8IBF4</u> _PLAF7	Hypothetical protein MAL7P1.167 [MAL7P1.167] [Pl	4.8	5e-04
	tr <u>Q7WRP2</u> _CLOBU	Botulinum neurotoxin type E (Fragment) [bont/E]	45	0.003
	tr <u>Q6DN58</u> _KLULA	COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (	45	0.004
	tr <u>Q815X3</u> _PLAF7	Hypothetical protein [PFL0360c] [Plasmodium falc	44	0.008
	tr <u>Q7RP92</u> _PLAYO	Clp [PY01567] [Plasmodium yoelii yoelii]	44	0.010
	tr <u>Q7RDL0</u> _PLAYO	Hypothetical protein [PY05412] [Plasmodium yoeli	44	0.010
	tr <u>Q6LFF0</u> _PLAF7	Hypothetical protein [PFF0575c] [Plasmodium falc	44	0.010
	tr <u>Q8IDG1</u> _PLAF7	Hypothetical protein PF13_0283 [PF13_0283] [Plas	43	0.013
<b></b>	tr <u>Q8I3X5</u> _PLAF7	Hypothetical protein PFE0655w [PFE0655w] [Plasmo	43	0.013
	tr <u>Q7RJM7</u> _PLAYO	Hypothetical protein [PY03232] [Plasmodium yoeli	43	0.013
	tr <u>Q9EMF0</u> AMEPV	AMV256 [AMV256] [Amsacta moorei entomopoxvirus (	42	0.022
		Hypothetical protein [PF11_0168] [Plasmodium fal	42	0.029
	tr <u>Q7RB20</u> _PLAYO	Hypothetical protein [PY06328] [Plasmodium yoeli	<u>42</u>	0.029
		Hypothetical protein [Dictyostelium discoideum (	<u>42</u>	0.037
<u> </u>		Hypothetical protein (Fragment) [PY00072] [Plasm		0.037
		Arabinogalactan protein [PY04751] [Plasmodium yo		0.064
		Hypothetical protein [PF14_0206] [Plasmodium fal	40	0.083
	——————————————————————————————————————		40	0.083
	<del>-</del>			0.083
		Hypothetical protein (Fragment) [PY01338] [Plasm	<u>40</u>	0.083
		NGA Mitochondrial ribosomal protein VAR1 [VAR1]	<u>40</u>	0.11
		Hypothetical protein [PF11_0326] [Plasmodium fal	40	0.11
		Hypothetical protein PFI1210w [PFI1210w] [Plasmo	40	0.11
		Hypothetical protein [PY01225] [Plasmodium yoeli	40	0.11
		Hypothetical protein [PFF0460w] [Plasmodium falc	40	0.14
		CPU Mannitol-1-phosphate 5-dehydrogenase (EC 1	<u>39</u>	0.19
1!	tr <u>Q81D18</u> PLAF7	Hypothetical protein MAL13P1.349 [MAL13P1.349] [	<u>39</u>	0.19

#### Graphical overview of the alignments

Click here to resubmit your query after masking regions matching <a href="PROSITE">PROSITE</a> profiles or <a href="Pfam">Pfam</a> HMMs</a>
(\*\* Help) (use <a href="ScanProsite">ScanProsite</a> for more details about PROSITE matches)

Profile hits

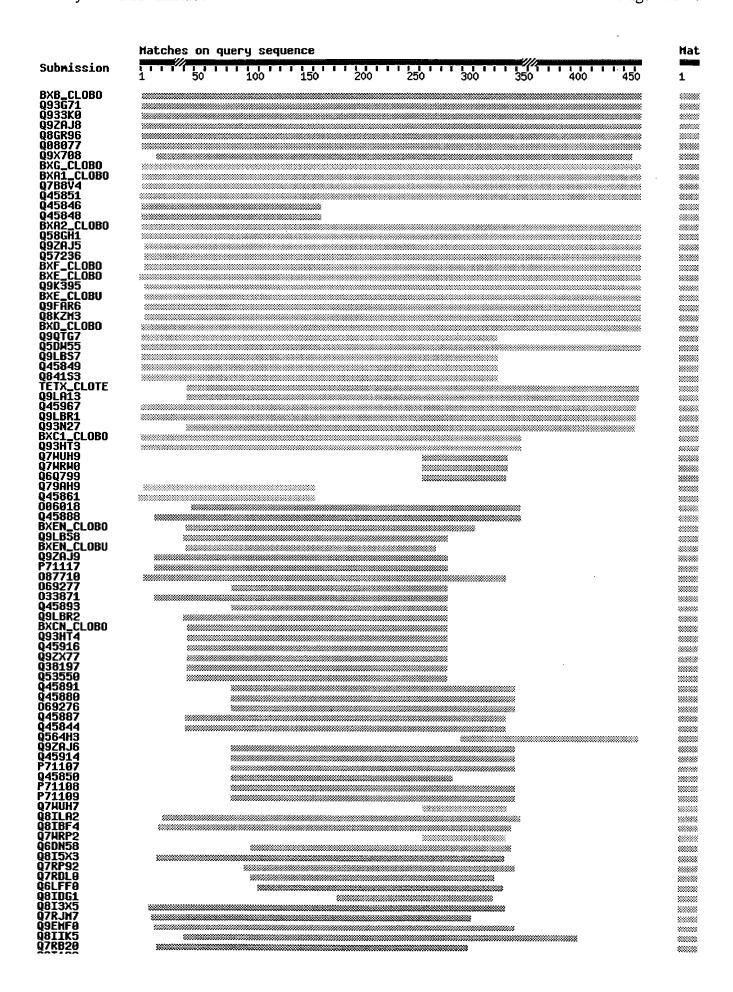
Pfam hits

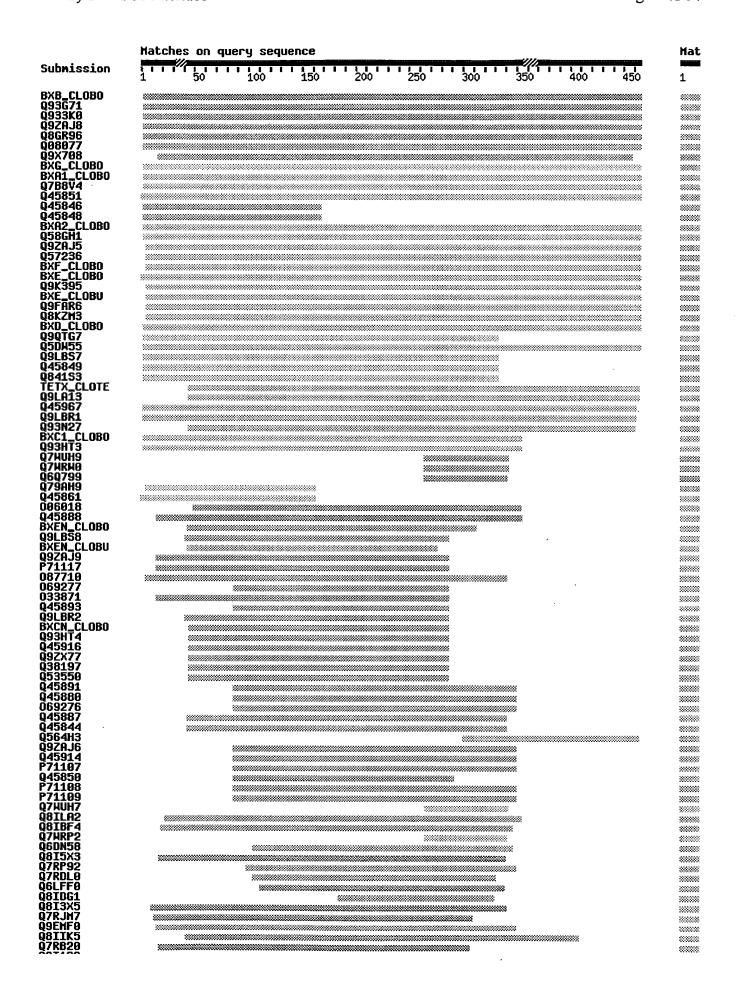
Toxin\_R\_bind\_N Toxin\_R\_bind\_C

## Graphical overview of the alignments

Click here to	resub	omit yo	ur query	after	masking	regions	matching	PROSITE	profiles
(%	« <u>нетр</u>	) (use	ScanPros	ite fo.	r more	detalls	about PRO	SITE mate	nes)

Profile hits	
Pfam hits	Toxin_R_bind_K Toxin_R_bind_C





## Alignments

sp P10 BXB	844 _CLOB	Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BoNT/B) (Bontoxilysin B) [botB] [Clostridium botulinum]	1290 AA align
Score	= 90	05 bits (2339), Expect = 0.0	
		= 441/463 (95%), Positives = 441/463 (95%)	
Query:	3	NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY NKYLKTIMPFDLSIYTNDTILIEMFNKYNSE RYKDNNLIDLSGYGAKVEVY	62
Sbjct:	828	NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVY	887
Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN	122
Sbjct:	888	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN	947
Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTIINCMENNSGWKISIRGNRIIWTLIDINGETKSVFFEYNIREDISEYINRWFFVTIT	182
Sbjct:	948	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	1007
Query:	183	NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	242
Sbjct:	1008	NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	1067
Query:	243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	302
Sbjct:	1068	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	1127
Query:	303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYT	362
Sbjct:	1128	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKK	1187
Query:	363	XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	422
Sbjct:	1188	EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	1247
Query:	423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE	
Sbjct:	1248	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 1290	
	93G71 93G71	Neurotoxin type B [Clostridium botulinum] 129CLOBO ali	1 AA gn
		53 bits (2204), Expect = 0.0 = 414/463 (89%), Positives = 429/463 (92%)	
Query:	3	NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY +KYLKT +PFDLS YTN+TILIE+FNKYNS+ RY+DN LIDLSGYGAKVEVY	62
Sbjct:	829	DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY	888
Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN DGV+LNDKNQFKLTSSANSKIRV QNQNIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHN	122
Sbjct:	889	The second secon	948

## Alignments

sp P108 BXB_	44 CLOBO	Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BoNT/B) (Bontoxilysin B) [botB] [Clostridium botulinum]	1290 AA <u>align</u>
		bits (2339), Expect = 0.0	
Identit	ties =	441/463 (95%), Positives = 441/463 (95%)	
Query: 3		KYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVY KYLKTIMPFDLSIYTNDTILIEMFNKYNSE RYKDNNLIDLSGYGAKVEVY	62
Sbjct: 8	328 N	KYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVY	887
Query: 6		GVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN	122
Sbjct: 8		GVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN	947
Query: 1		YTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	182
Sbjct: 9		YTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	1007
Query: 1		NLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NLWNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	242
Sbjct: 1		NLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	1067
Query: 2		NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN NIEERYKIOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	302
Sbjct: 1		NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	1127
Query: 3		NSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX NSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNOEWRVYT	362
Sbjct: 1		NSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKK	1187
Query: 3	363 X	XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	422
Sbjct: 1	1188 E	EEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	1247
Query: 4		FEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 FEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE	
Sbjct: 1		FEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 1290	
	3 <u>G71</u> 3G71_0	** · · · · · · · · · · · · · · · · · ·	1 AA gn
		bits (2204), Expect = 0.0 414/463 (89%), Positives = 429/463 (92%)	
Query: 3		KYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY KYLKT +PFDLS YTN+TILIE+FNKYNS+ RY*DN LIDLSGYGAKVEVY	62
Sbjct: 8		KYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY	888
Query: 6		GVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN GV+LNDKNQFKLTSSANSKIRV QNQNIIFNS+FLDESVSFWIRIPKYKNDGIQNYIHN	122
Sbjct: 8		GVKLNDKNQFKLTSSANSKIRVIQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN	948

Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTIINCMKNNSGWKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT	182
Sbjct:	949	EYTI`INCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT	1008
Query:	183	NNLNNAKIYINGKLESHTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ	242
Sbjct:	1009	NNSDNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ	1068
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Sbjct:	1069	SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	1128
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Sbjct:	1129	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYIYKYFKK	1188
Query:	363	XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	422
Sbjct:	1189	EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	1248
Query:	423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 VF+EYKDYFCISKWYLKEVKRKPYN KLGCNWQFIPKDEGWTE	
Sbjct:	1249	VFKEYKDYFCISKWYLKEVKRKPYNSKLGCNWQFIPKDEGWTE 1291	

```
Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
            +KYLKT +PFDLS YTN+TILIE+FMKYNS+
                                                   RY+DN LIDLSGYGAKVEVY
Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY 888
Query: 63
           DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
           DGV+LNDKNQFKLTSSANSKIRVTQNQNIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHN
Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN 948
Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           EYTTINCMKNNSGWKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTTT
Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT 1008
Query: 183 NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242
           NN +NAKIYINGKLES+ DI+DIREVIAN ELIFKLDG+IDRTQFIWMKYFSIFNTELSQ
Sbjct: 1009 NNSDNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068
Query: 243 SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
            SNIEE YKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYN
Sbjct: 1069 SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYN 1128
Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX 362
            QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNINQEWRVY
Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYMYKYFKK 1188
```

Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTIINCMKNNSGWKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT	182
Sbjct:	949	EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT	1008
Query:	183	NNLNNAKIYINGKLESHTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NN +NAKIYINGKLESH DIHDIREVIAN ETTEKLDGHIDRTQFIWMKYFSIFNTELSQ	242
Sbjct:	1009	NNSDNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ	1068
Query:	243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN SNIEE YKIQSYSEYLKDEWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	302
Sbjct:	1069	SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	1128
Query:	303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVY	362
Sbjct:	1129	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYIYKYFKK	1188
Query:	363	XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	422
Sbjct:	1189	EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	1248
Query:	423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 VF+EYKDYFCISKWYLKEVKRKPYN KLGCNWQFIPKDEGWTE	
Sbjct:	1249	VFKEYKDYFCISKWYLKEVKRKPYNSKLGCNWQFIPKDEGWTE 1291	

tr	<u>Q933K0</u>	Type B cryptic neurotoxin [Clostridium	1291 AA
	Q933K0 CLOBO	botulinum]	align

Score = 852 bits (2202), Expect = 0.0 Identities = 414/463 (89%), Positives = 429/463 (92%)

Query:	3	NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	62
Sbjct:	829	+KYLKT +PFDLS YTN+TILIE+FNKYNS+ RY+DN LIDLSGYGAKVEVY DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY	888
Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN DGV+LNDKNQFKLTSSANSKIRVTQNQNIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHN	122
Sbjct:	889	DGVKLNDKNQFKLTSSANSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN	948
Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTTINCMKNNSGWKISIRGN IIWTLIDINGK KSVFSEY+T+EDISEYINRWFFVTIT	182
Sbjct:	949	EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT	1008
Query:	183	NNLNNAKIYINGKLESHTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTOFIWMKYFSIFNTELSO	242
Sbjct:	1009	· ·	1068
Query:	243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN SNIEE YKIOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYN	302
Sbjct:	1069	SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYN	1128
Query:	303	QNSKYINYRDLYIGEKFIIRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVY	362
Sbjct:	1129	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYMYKYFKK	1188

```
Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 422
                  apisdsdefyntiqikeydeqptyscqllfkkdeestdeigligihrfyesgi
Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 1248
Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
           VF+EYKDYFCISKWYLKEVKRKPYN KLGCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYNSKLGCNWQFIPKDEGWTE 1291
                                                                      1291 AA
tr
     Q9ZAJ8
                         BonT protein [bonT] [Clostridium
     Q9ZAJ8_CLOBO
                                                                      align
Score = 850 bits (2196), Expect = 0.0
Identities = 413/463 (89%), Positives = 428/463 (92%)
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
           +KYLET +PEDLS YTN+TILIE+FNKYMS+
                                                   RY+DN LIDLSGYGAKVEVY
Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY 888
Query: 63
           DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
           DGV+LNDENQEKLTSSANSKIRV QNQNIIFNS+FLDESVSFWIRIPEYENDGIQNYIHN
Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVIQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN 948
Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           EYTIINCMKNNSGWKISIRGN TIWTHIDINGK KSVFFEY+I+EDISEYINEWFFVTIT
Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT 1008
Query: 183 NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242
           NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ
Sbjct: 1009 NNSDNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068
Query: 243 SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
           SNIEE YKIGSYSEYLKDEWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYN
Sbjct: 1069 SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYN 1128
Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX 362
           QNSKYINYRDLYLGEKFIIRRKSNSQSINDDIVRKEDYTYLDFFNLNQEWRVY
Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYMYKYFKK 1188
Query: 363 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 422
                  APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 1248
Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
           VF+EYKDYFCISEWYLKEVKRKPYN KLGCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYNSKLGCNWQFIPKDEGWTE 1291
     Q8GR96
tr
                         Neurotoxin [bontb] [Clostridium botulinum] 1291 AA
     Q8GR96_CLOBO
                                                                      align
Score = 831 bits (2146), Expect = 0.0
Identities = 403/463 (87%), Positives = 423/463 (91%)
```

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62

```
Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 422
                   APISDSDEFYNTIQIKEYDEQPTYSCQLLEKKDEESTDEIGLIGIHREYESGI
Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 1248
Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
            VF+EYKDYFCISKWYLKEVKRKPYN KLGCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYNSKLGCNWQFIPKDEGWTE 1291
tr
     Q9ZAJ8
                           BonT protein [bonT] [Clostridium
                                                                       1291 AA
     Q9ZAJ8 CLOBO
                          botulinum
                                                                       align
 Score = 850 \text{ bits } (2196), \text{ Expect = } 0.0
 Identities = 413/463 (89%), Positives = 428/463 (92%)
            NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
Query: 3
            +KYLET +PEDLS YTN+TILIE+FNKYNS+
                                                    RY+DN LIDLSGYGAKVEVY
Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY 888
Query: 63
            DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
            DGV+LNDFNQEKLTSSANSKIRV QNQNIIENS+FLDESVSFWIRIPFYKNDGIQNYIHN
Sbjct: 889 DGVKLNDKNOFKLTSSANSKIRVIONONIIFNSMFLDFSVSFWIRIPKYKNDGIONYIHN 948
Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
            EYTIINCMKNNSGWKISIRGN TIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT
Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT 1008
Query: 183 NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242
            NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ
Sbjct: 1009 NNSDNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068
Query: 243 SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
            SNIEE YKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYN
Sbjct: 1069 SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYN 1128
Query: 303 ONSKYINYRDLYIGEKFIIRRKSNSOSINDDIVRKEDYIYLDFFNLNOEWRVYTXXXXXX 362
            QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFWLMQEWRVY
Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYMYKYFKK 1188
Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 422
                   APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIERFYESGI
Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 1248
Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
            VE+EYKDYFCISKWYLKEVKRKPYN KLGCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYNSKLGCNWQFIPKDEGWTE 1291
     Q8GR96
                           Neurotoxin [bontb] [Clostridium botulinum] 1291 AA
     Q8GR96 CLOBO
                                                                       align
 Score = 831 bits (2146), Expect = 0.0
 Identities = 403/463 (87%), Positives = 423/463 (91%)
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
```

Sbjct: 829	+K+LKTI+PFDLS+YTN+TILIE+FNKYNSE RY+DNNLIDLSGYGA VEVY DKHLKTIIPFDLSMYTNNTILIEIFNKYNSEILNNIILNLRYRDNNLIDLSGYGANVEVY	888
Query: 63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN	
Sbjct: 889	DGVELNDKNQFKLTSS NS+1RVTQNQN11FNS+FLDFSVSFW1R1PKYKNDG1QNY1HN DGVELNDKNQFKLTSSTNSEIRVTQNQN11FNSMFLDFSVSFW1R1PKYKNDG1QNY1HN	948
Query: 123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTIINC+KNNSGWKISIRGNRIIWTL DINGKTKSVFFEY+IREDIS+YINRWFFVTIT	182
Sbjct: 949	EYTIINCIKNNSGWKISIRGNRIIWTLTDINGKTKSVFFEYSIREDISDYINRWFFVTIT	1008
Query: 183	NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NN +NAKIYINGKLESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	242
Sbjct: 100	9 NNSDNAKIYINGKLESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	1068
Query: 243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN SNI+E YKIOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYN	302
Sbjct: 106	9 SNIKEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYN	1128
Query: 303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX QNS YINYR+LYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFN N+EWRVY	362
Sbjct: 112	9 QNSNYINYRNLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRVYAYKDFKE	1188
Query: 363	XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI A I DS+EFY TIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	422
Sbjct: 118	EEKKLFLANIYDSNEFYKTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	1248
Query: 423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 V *+YK+YFCISKWYLKEVKRKPYN LGCNWQFIPKDEGW E	
Sbjct: 124	9 VLKDYKNYFCISKWYLKEVKRKPYNPNLGCNWQFIPKDEGWIE 1291	
tr <u>00807</u>	BONT/B [bont/b] [Clostridium botulinum] 1291	AA

tr <u>Q08077</u> **BONT/B [bont/b] [Clostridium botulinum]** 1291 AA Q08077\_CLOBO <u>align</u>

Score = 800 bits (2067), Expect = 0.0 Identities = 387/463 (83%), Positives = 416/463 (89%)

Query:	3	${\tt NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY}$	62
		+KYLKTI+PFDLS Y+N ILI++FNKYNSE RY+DNNLIDLSGYGAKVEVY	
Sbjct:	829	DKYLKTIIPFDLSTYSNIEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY	888
Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN	122
		DGV+LNDKNQEKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYIHN	
Sbjct:	889	DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN	948
Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	182
		EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVYFEYNIREDISEYINRWFFVTIT	
Sbjct:	949	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	1008
Query:	183	${\tt NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ}$	242
		NNT+WWKIAING FERN DIKDI EAI WGEI EKTDGD+DELÖEIMWKAERIENI+F+Ö	
Sbjct:	1009	NNLDNAKIYINGTLESNMDIKDIGEVIVNGEITFKLDGDVDRTQFIWMKYFSIFNTQLNQ	1068
Query:	243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	302
		SNI+E YKIQSYSEYLKDEWGNPLMYNKEYYMFNAGNKNSYIKL KDS VGEIL RSKYN	

		+K+LKTI+PFDLS+YTN+TTLTE+FNKYNSE RY+DNNLIDLSGYGA VEVY	
Sbjct:	829	DKHLKTIIPFDLSMYTNNTILIEIFNKYNSEILNNIILNLRYRDNNLIDLSGYGANVEVY	888
Query:	63	DGVELNDKNOFKLTSSANSKIRVTQNONIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN DGVELNDKNOFKLTSS NS+IRVTONONIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHK	122
Sbjct:	889	DGVELNDKNQFKLTSSTNSEIRVTQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN	948
Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTTINC+KNNSGWKISIRGNRIIWTL DINGKTKSVFFEY+TREDIS+YTNRWFFVTIT	182
Sbjct:	949	EYTIINCIKNNSGWKISIRGNRIIWTLTDINGKTKSVFFEYSIREDISDYINRWFFVTIT	1008
Query:	183	NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NN +NAKIYINGKLESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	242
Sbjct:	1009	NNSDNAKIYINGKLESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	1068
Query:	243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN SNI+E YKIOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYN	302
Sbjct:	1069	SNIKETYKTOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYTKLKKDSSVGETLTRSKYN	1128
Query:	303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX QNS YINYR+LYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFN N+EWRVY	362
Sbjct:	1129		1188
Query:	363	XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI A I DS+EFY TIOIKEYDEOPTYSCOLLFKKDEESTDEIGLIGIHRFYESGI	422
Sbjct:	1189	EEKKLFLANIYDSNEFYKTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI	1248
Query:	423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 V ++YK+YFCISKWYLKEVKRKPYN LGCNWQFIPKDEGW E	
Sbjct:	1249	VLKDYKNYFCISKWYLKEVKRKPYNPNLGCNWQFIPKDEGWIE 1291	

tr <u>Q08077</u> **BoNT/B [bont/b] [Clostridium botulinum]** 1291 AA <u>align</u>

Score = 800 bits (2067), Expect = 0.0 Identities = 387/463 (83%), Positives = 416/463 (89%)

Query:	3	NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY +KYLKTI+PFDLS Y+N ILI++FNKYNSE RY+DNNLIDLSGYGAKVEVY	62
Sbjct:	829	DKYLKTIIPFDLSTYSNIEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY	888
Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IONYIHN	122
Sbjct:	889	DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN	948
Query:	123	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	182
Sbjct:	949	EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT	1008
Query:	183	NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ NNL+NAKIYING LESN DIKDI EVI NGEI FKLDGD+DRTQFIWMKYFSIFNT+L+Q	242
Sbjct:	1009	NNLDNAKIYINGTLESNMDİKDIGEVIVNGEITFKLDGDVDRTQFIWMKYFSIFNTQLNQ	1068
Query:	243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN SNI+E YKIGSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKL KDS VGEIL BSKYN	302

Sbjct:	1069	SNIKEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILIRSKYN	1128
Query:	303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX QNS YINYR+LYIGEKFIIRR+SNSQSINDDIVRKEDYI+LD ++EWRVY	362
Sbjct:	1129	QNSNYINYRNLYIGEKFIIRRESNSQSINDDIVRKEDYIHLDLVLHHEEWRVYAYKYFKE	1188
Query:	363	XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI + ISDS+EFY TI+IKEYDEQF+YSCQLLFKKDEESTD+IGLIGIHRFYESG+	
Sbjct:	1189	QEEKLFLSIISDSNEFYKTIEIKEYDEQPSYSCQLLFKKDEESTDDIGLIGIHRFYESGV	
Query:	423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 + ++YKDYFCISKWYLKEVKRKPY LGCNWQFIPKDEGWTE	
Sbjct:	1249	LRKKYKDYFCISKWYLKEVKRKPYKSNLGCNWQFIPKDEGWTE 1291	
tr <u>Q9X</u> Q9X		Botulinum neurotoxin type B (Fragment) [boNT/B] CLOBO [Clostridium botulinum]	441 AA <u>align</u>
		91 bits (2043), Expect = 0.0 = 385/441 (87%), Positives = 402/441 (90%)	
Query:		YTNDTILIEMFNKYNSEXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT YTN+TILIE+FNKYNS+ RY+DNNLIDLSGYGA VEVYDGVELNDKNQFKLT	76 _
Sbjct:		YTNNTILIEIFNKYNSKILNNIILNLRYRDNNLIDLSGYGANVEVYDGVELNDKNQFKLT	60
Query:		SSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGW SS NS+IRVTQNQNIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINC+KNNSGW	136
Sbjct:		SSTNSEIRVTQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCIKNNSGW	120
Query:		KISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKL KISIRGNRIIWTL DINGKTKSVFFEY+TREDIS+YINRWFFVTITNN +NAKIYINGKL	196
Sbjct:		KISIRGNRIIWTLTDINGKTKSVFFEYSIREDISDYINRWFFVTITNNSDNAKIYINGKL	180
Query:		ESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSE ESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNI+E YKIQSYSE	256
Sbjct:		ESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIKEIYKIQSYSE	240
Query:		YLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIG YLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR+LYIG	316
Sbjct:		YLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIG	300
Query:		EKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXXAPISDSD	376
Sbjct:		EKFIIRRKSNSQSINDDIVRKEDYIYLDFFN N+EWRVY A I DS+ EKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRVYAYKDFKEEEKKLVLANIYDSN	360
Query:		EFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKW	436
Sbjct:		EFY TIQIKEYDEQFTYSCQLLFKKDEESTDEIGLIGIHRFYESGIV ++YK+YFCISKW EFYKTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVLKDYKNYFCISKW	420
Query:		YLKEVKRKPYNLKLGCNWQFI 457	
Sbjct:		YLKEVKRKPYN LGCNWQFI YLKEVKRKPYNPNLGCNWQFI 441	

Sbjct:	1069	SNIKEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILIRSKYN	1128
Query:	303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXX QNS YINYR+LYIGEKFIIRR+SNSQSINDDIVRKEDYI+LD ++EWRVY	362
Sbjct:	1129	QNSNYINYRNLYIGEKFIIRRESNSQSINDDIVRKEDYIHLDLVLHHEEWRVYAYKYFKE	1188
Query:	363	XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI + ISDS+EFY TI+IKEYDEQF+YSCQLLFKKDEESTD+IGLIGIHRFYESG+	
Sbjct:	1189	QEEKLFLSIISDSNEFYKTIEIKEYDEQPSYSCQLLFKKDEESTDDIGLIGIHRFYESGV	
Query:	423	VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 + +++YKDYFCISKWYLKEVKRKPY LGCNWQFIPKDEGWTE	
Sbjct:	1249	LRKKYKDYFCISKWYLKEVKRKPYKSNLGCNWQFIPKDEGWTE 1291	
tr <u>Q9X</u> Q9X		Botulinum neurotoxin type B (Fragment) [boNT/B] CLOBO [Clostridium botulinum]	441 AA align
		91 bits (2043), Expect = 0.0 = 385/441 (87%), Positives = 402/441 (90%)	
Query:		YTNDTILIEMFNKYNSEXXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT YTN+TILIE+FNKYNS+ RY+DNNLIDLSGYGA VEVYDGVELNDKNQFKLT	76
Sbjct:		YTNNTILIEIFNKYNSKILNNIILNLRYRDNNLIDLSGYGANVEVYDGVELNDKNQFKLT	60
Query:		SSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGW SS NS+IRVTQNQNIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINC+KNNSGW	136
Sbjct:		SSTNSEIRVTQNQNIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCIKNNSGW	120
Query:		KISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKL KISIRGNRIIWTL DINGKTKSVFFEY+IREDIS+YINRWFFVTITNN +NAKIYINGKL	196
Sbjct:		KISIRGNRIIWTLTDINGKTKSVFFEYSIREDISDYINRWFFVTITNNSDNAKIYINGKL	180
Query:		ESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSE ESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIENTELSQSNI+E YKIQSYSE	256
Sbjct:		ESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIKEIYKIQSYSE	240
Query:		YLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIG YLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR÷LYIG	316
Sbjct:		YLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIG	300
Query:		EKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXAPISDSD EKFIIRRKSNSOSINDDIVRKEDYIYLDFFN N+EWRVY A I DS+	376
Sbjct:		EKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRVYAYKDFKEEEKKLVLANIYDSN	360
Query:		EFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKW EFY TIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIV ++YK+YFCISKW	436
Sbjct:		EFYKTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVLKDYKNYFCISKW	420
Query:		YLKEVKRKPYNLKLGCNWQFI 457 YLKEVKRKPYN LGCNWQFI	
Sbict:		YLKEVKRKPYNPNLGCNWOFI 441	

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sp Q60393
              Botulinum neurotoxin type G precursor (EC 3.4.24.69)
                                                                         1296
    BXG CLOBO (BoNT/G)
                                                                         AΑ
              (Bontoxilysin G) [botG] [Clostridium botulinum]
                                                                         align
 Score = 468 \text{ bits (1203), Expect} = e-130
 Identities = 230/469 (49%), Positives = 324/469 (69%), Gaps = 11/469 (2%)
Query: 3
            NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
            N++LK +PFDLS+YT DTTLI++FN Y S
                                                    X +
                                                         LID SGYGA + V
Sbjct: 833 NRHLKDSIPFDLSLYTKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVG 892
            DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
Query: 63
                       QYKL +S NS I Q++ ++++S+F +FS++FW+B PKY N+ IQ Y+
Sbjct: 893 SDVIFNDIGNGQFKLNNSENSNITAHQSKFVVYDSMFDNFSINFWVRTPKYNNNDIQTYL 952
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
             NEYTII+C+KN+SGWK+SI+GNRIIWTLID+N K+KS+FFEY+I+++IS+YIN+WF +T
Sbjct: 953 QNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSIFFEYSIKDNISDYINKWFSIT 1012
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
            ITN+ L NA IYING L+ + I ++ + ++ FKL
                                                      D T*F+W+K F*IF E
Sbjct: 1013 ITNDRLGNANIYINGSLKKSEKILNLDRINSSNDIDFKLINCTDTTKFVWIKDFNIFGRE 1072
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
            L+ + +
                   Y IQS + LEDFWGNPL Y+ +XY+FM G +N YIK
Sbjct: 1073 LNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRT 1132
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-WRVYTX 357
             +N + INY++LY+G +FTI++ SNS++I ND+IVR+ DYIYL+ N++ E +RVY
Sbjct: 1133 NFNNAA--INYQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVL 1190
Query: 358 XXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRF 417
                       APT+D
                               FY+ +QIK+Y E+ TY+CQ+L +KD T
Sbjct: 1191 VNSKEIQTQLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKD---TKTFGLFGIGKF 1247
Query: 418 YES-GIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
            + G V++ Y +YFCIS+WYL+ + L+LGCNWQFIP DEGWTE
Sbjct: 1248 VKDYGYVWDTYDNYFCISQWYLRRISENINKLRLGCNWQFIPVDEGWTE 1296
sp P10845
              Botulinum neurotoxin type A precursor (EC 3.4.24.69)
                                                                         1295
   BXA1 CLOBO (BoNT/A)
                                                                         AΑ
               (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin
                                                                         align
              A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
               [Clostridium botulinum]
 Score = 316 \text{ bits } (810), \text{ Expect} = 6e-85
 Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXXXXXXXXXXX 62
Query: 3
           N L T +PF LS Y ++ L+ F +Y
                                                   RY* N+LIDLS Y +K+ *
Sbjct: 841 NNTLSTDIPFQLSKYVDNQRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIG 900
           DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
Query: 63
             V + DRNQ +L + +SKI V
                                         I++NS++ +FS SEWIRLPRY N
Sbjct: 901 SKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 958
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sp Q60393 Botulinum neurotoxin type G precursor (EC 3.4.24.69) 1296 BXG CLOBO (BoNT/G) AA (Bontoxilysin G) [botG] [Clostridium botulinum] align Score = 468 bits (1203), Expect = e-130Identities = 230/469 (49%), Positives = 324/469 (69%), Gaps = 11/469 (2%) Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62 N++LK +PFDLS+YT DTILI++FN Y S  $\chi +$ LID SGYGA + V Sbjct: 833 NRHLKDSIPFDLSLYTKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVG 892 Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120 QFKL +S NS I Q++ ++++S+F +FS++FW+F PKY N+ IQ Y+ Sbjct: 893 SDVIFNDIGNGQFKLNNSENSNITAHQSKFVVYDSMFDNFSINFWVRTPKYNNNDIQTYL 952 Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180 NEYTII+C+KN+SGWK+SI+GNRIIWTLID+N K+KS+FFEY+I+++IS+YIN+WF +T Sbjct: 953 QNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSIFFEYSIKDNISDYINKWFSIT 1012 Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTE 239 ITN+ L NA IYING L+ + I ++ + ++ +I FKL D T\*F+W+K F\*IF E Sbjct: 1013 ITNDRLGNANIYINGSLKKSEKILNLDRINSSNDIDFKLINCTDTTKFVWIKDFNIFGRE 1072 Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299 L+ + + Y IQS + LEDFWGNPL Y+ +YY+FN G +N YIK + +GE Sbjct: 1073 LNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRT 1132 Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-WRVYTX 357 +N + INY++LY+G +FII++ SNS++I ND+IVR+ DYIYL+ N++ E +RVY Sbjct: 1133 NFNNAA--INYQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVL 1190 Query: 358 XXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRF 417 APT+D FY+ +QIK+Y E+ TY+CQ+L +KD T Sbjct: 1191 VNSKEIQTQLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKD---TKTFGLFGIGKF 1247 Query: 418 YES-GIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 + G V++ Y +YECIS+WYL+ + L+LGCNWQFIP DEGWTE Sbjct: 1248 VKDYGYVWDTYDNYFCISQWYLRRISENINKLRLGCNWQFIPVDEGWTE 1296 sp P10845 1295 Botulinum neurotoxin type A precursor (EC 3.4.24.69) BXA1 CLOBO (BoNT/A) align (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain] [botA] [Clostridium botulinum] Score = 316 bits (810), Expect = 6e-85Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%) Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62 N L T +PF LS Y ++ L+ F +Y RY\* N+LIDLS Y +K+ \* Sbjct: 841 NNTLSTDIPFQLSKYVDNQRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIG 900 Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120 V + DKNQ +L + +SKI V I++NS++ +FS SEWIRIPKY N Sbjct: 901 SKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 958

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Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
          NEYTIINCM+NNSGWK+S+ IIWTL D + V F+Y+ +1S+YINRW FVT
Sbjct: 959 -NEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1017
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
          Sbjct: 1018 ITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE 1077
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
          L++ I++ Y QS S LKDEWG+ L Y+K YYM N + N Y+ +
Sbjct: 1078 LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKG 1137
Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNO 350
          P G ++T + Y +S LY G KFII++ ++ D+IVR D +Y++ N+
Sbjct: 1138 PRGSVMTTNIYLNSS-----LYRGTKFIIKKYASGN--KDNIVRNNDRVYINVVVKNK 1188
Query: 351 EWRVYTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409
          E+R+T I D + +K ++Q T C++ + + ++I
Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKM--NLQDNNGNDI 1246
Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
          G IG H+F S WY ++++R + LGC+W+FIP D+GW E
Sbjct: 1247 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSWEFIPVDDGWGE 1292
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tr <u>Q7B8V4</u> BoNT/A [bont/a] [Clostridium botulinum] 1296 AA Q7B8V4\_CLOBO align

```
Score = 316 bits (810), Expect = 6e-85
Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)
Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
          N L T +PF LS Y ++ L+ F +Y RY+ N+LIDLS Y +K+ +
Sbjct: 842 NNTLSTDIPFQLSKYVDNQRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIG 901
Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
           V + DKNQ +L + +SKI V I++NS++ +FS SEWIRIPKY N N
Sbjct: 902 SKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 959
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
          NEYTIINCM*NNSGWK+S* IIWTL D + V F+Y* +IS*YINRW FVT
Sbjct: 960 -NEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1018
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
          ITNN LNN+KIYING+L I ++ + A* I+FKLDG D **IW+KYF*+F+ E
Sbjct: 1019 ITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE 1078
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
          L++ I++ Y QS S LKDFWG+ L Y+K YYM N + N Y+ +
Sbjct: 1079 LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKG 1138
Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
           Sbjct: 1139 PRGSVMTTNIYLNSS-----LYRGTKFIIKKYASGN--KDNIVRNNDRVYINVVVKNK 1189
```

Query: 351 EWRVYTXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409

```
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
          NEXTIINCM+NNSGWE+S+ LIWTL D + V F+Y+ +IS+YINRW FVT
Sbjct: 959 -NEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1017
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           Sbjct: 1018 ITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE 1077
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
           L++ I++ Y QS S LKDFWG+ L Y+K YYM N + N Y+ +
Sbjct: 1078 LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKG 1137
Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNO 350
           P G ++T + Y +S LY G KFII++ ++ D+IVR D +Y++ N+
Sbjct: 1138 PRGSVMTTNIYLNSS-----LYRGTKFIIKKYASGN--KDNIVRNNDRVYINVVVKNK 1188
Query: 351 EWRVYTXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409
          E+R+T ID ++K ++Q T C++ ++++I
Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKM--NLQDNNGNDI 1246
Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
           G IG H+F S WY ++++R + LGC+W+FIP D+GW E
Sbjct: 1247 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSWEFIPVDDGWGE 1292
tr
     Q7B8V4
                       BoNT/A [bont/a] [Clostridium botulinum] 1296 AA
     Q7B8V4 CLOBO
Score = 316 bits (810), Expect = 6e-85
Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)
Query: 3
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
          N L T +PF LS Y ++ L+ F +Y RY+ N+LIDLS Y +K+ +
Sbjct: 842 NNTLSTDIPFQLSKYVDNQRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIG 901
Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
           V + DKNQ +L + +SKT V I++NS++ +FS SFWIRIPKY N N
Sbjct: 902 SKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 959
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
          NEYTIINCM*NNSGWK+S* IIWTL D + V F+Y* +IS*YINRW FVT
Sbjct: 960 -NEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1018
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
          ITNN LAW+KIYING+L I ++ + A+ I+FKLDG D ++IW+KYF++F+ E
Sbjct: 1019 ITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE 1078
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
          L++ I++ Y QS S LKDFWG+ L Y+K YYM N + N Y+ +
Sbjct: 1079 LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKG 1138
Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
          P G ++T + Y +S LY G KETI++ ++ D+TVR D +X++
Sbjct: 1139 PRGSVMTTNIYLNSS-----LYRGTKFIIKKYASGN--KDNIVRNNDRVYINVVVKNK 1189
```

Query: 351 EWRVYTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409

```
I D + +K ++Q T C++ + + ++T
          2+2+ T
Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKM--NLQDNNGNDI 1247
Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
          G IG S+F S WY ++++R + LGC+W+FIP D+GW E
Sbjct: 1248 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSWEFIPVDDGWGE 1293
    Q45851
                                                              1268 AA
                      Neurotoxin type F [bont /f] [Clostridium
    Q45851 9CLOT baratii]
                                                                align
Score = 301 \text{ bits } (771), \text{ Expect = } 2e-80
Identities = 179/471 (38%), Positives = 270/471 (57%), Gaps = 32/471 (6%)
Query: 1
          MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVE 60
                                                +Y++N ID SGYG+ +
          + + L +PF+LS YTND ILI + ++
Sbjct: 824 LVSNTLNNSIPFELSEYTNDKILIHILIRFYKRIIDSSILNMKYENNRFIDSSGYGSNIS 883
Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
          + + + ++NQF + SS S++ +TQN II+NS + +FSVSFW+RIPKY N ++N
Sbjct: 884 INGDIYIYSTNRNQFGIYSSRLSEVNITQNNTIIYNSRYQNFSVSFWVRIPKYNN--LKN 941
Query: 119 YIHNEYTIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
          ++NEYTIINCM+NN SGWKIS+ N IIWTL D G + + F Y DIS+YIN+W
Sbjct: 942 -LNNEYTIINCMRNNNSGWKISLNYNNIIWTLQDTTGNNQKLVFNYTQMIDISDYINKWT 1000
Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
           Sbjct: 1001 FVTITNNRLGHSKLYINGNLTDQKSILNLGNIHVDDNILFKIVGCND-TRYVGIRYFKIF 1059
Query: 237 NTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEI- 295
          N EL ++ IE Y + S LKDFWGN L+YNK+YY+ N N + + K+S + I
Sbjct: 1060 NMELDKTEIETLYHSEPDSTILKDFWGNYLLYNKKYYLLNLLKPN--MSVTKNSDILNIN 1117
Query: 296 LTRSKYNONSKYINYRDLYIGEKFIIRRKSNSOSIN-DDIVRKEDYIYLDFFNLNOEWRV 354
            R Y++ + + N R LY G + TIR+ ++ + N D+ VRK D +Y++ + N E+++
Sbjct: 1118 RQRGIYSKTNIFSNAR-LYTGVEVIIRKVGSTDTSNTDNFVRKNDTVYINVVDGNSEYQL 1176
Query: 355 YTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGI 414
          Sbjct: 1177 YADVSTSAVEKTIKLRRISNSN--YNSNQMIIMDSIGD-NCTMNFKTN--NGNDIGLLGF 1231
Query: 415 HRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
          H + S WY K ++ N GC W FI K+ GW E
Sbjct: 1232 H-----LNNLVASSWYYKNIRNNTRN--NGCFWSFISKEHGWQE 1268
tr Q45846
             Botulinum neurotoxin type B (Fragment) [BoNT/B]
                                                                   361
   Q45846_CLOBO [Clostridium
                                                                   AA .
               botulinum]
                                                                    align
Score = 299 bits (765), Expect = 1e-79
Identities = 144/166 (86%), Positives = 155/166 (92%)
```

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62

```
I D + +K ++0 T C++ + + ++1
           2+2+ T
Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKM--NLQDNNGNDI 1247
Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWOFIPKDEGWTE 465
           G IG H+F S WY ++++R + LGC+W+FIP D+GW E
Sbjct: 1248 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSWEFIPVDDGWGE 1293
    <u>Q45851</u> Neurotox
Q45851_9CLOT baratii]
tr
                       Neurotoxin type F [bont /f] [Clostridium 1268 AA
                                                                  align
 Score = 301 \text{ bits } (771), \text{ Expect} = 2e-80
 Identities = 179/471 (38%), Positives = 270/471 (57%), Gaps = 32/471 (6%)
Query: 1
          MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVE 60
           + + L +PF+LS YTND ILI + ++
                                                  +Y++N ID SGYG+ +
Sbjct: 824 LVSNTLNNSIPFELSEYTNDKILIHILIRFYKRIIDSSILNMKYENNRFIDSSGYGSNIS 883
Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
          + + + ++NQF + SS S++ +TQN II+NS + +FSVSFW+RIPKY N ++N
Sbjct: 884 INGDIYIYSTNRNQFGIYSSRLSEVNITQNNTIIYNSRYQNFSVSFWVRIPKYNN--LKN 941
Query: 119 YIHNEYTIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
           ++NEYTIINCM+NN SGWKIS+ N IIWTL D G + + F Y DIS+YIN+W
Sbjct: 942 -LNNEYTIINCMRNNNSGWKISLNYNNIIWTLQDTTGNNQKLVFNYTQMIDISDYINKWT 1000
Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
           Sbjct: 1001 FVTITNNRLGHSKLYINGNLTDQKSILNLGNIHVDDNILFKIVGCND-TRYVGIRYFKIF 1059
Query: 237 NTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEI- 295
           N EL ++ IE Y + S LKDFWGN L+YNK+YY+ N N + + K+S + I
Sbjct: 1060 NMELDKTEIETLYHSEPDSTILKDFWGNYLLYNKKYYLLNLLKPN--MSVTKNSDILNIN 1117
Query: 296 LTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRV 354
            R Y++ + + N R LY G + IIR+ ++ + N D+ VRK D +Y++ + N E+++
Sbjct: 1118 RQRGIYSKTNIFSNAR-LYTGVEVIIRKVGSTDTSNTDNFVRKNDTVYINVVDGNSEYQL 1176
Query: 355 YTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGI 414
           Y IS+S+ YN+ Q+ D +C + FK + + ++IGL+G
Sbjct: 1177 YADVSTSAVEKTIKLRRISNSN--YNSNOMIIMDSIGD-NCTMNFKTN--NGNDIGLLGF 1231
Query: 415 HRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
          H + S WY K ++ N GC W FI K+ GW E
Sbjct: 1232 H-----LNNLVASSWYYKNIRNNTRN--NGCFWSFISKEHGWQE 1268
tr Q45846
               Botulinum neurotoxin type B (Fragment) [BoNT/B]
                                                                     361
   Q45846 CLOBO [Clostridium
                                                                     AΑ
               botulinum]
                                                                      align
Score = 299 \text{ bits } (765), \text{ Expect = } 1e-79
Identities = 144/166 (86%), Positives = 155/166 (92%)
Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
```

+KYLKTI+PFDLS+YTN+ TLI++FNKYNSE RY+DMNLIDLSGYGAKVEVY Sbjct: 196 DKYLKTIIPFDLSMYTNNEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255 Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122 DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYIHN Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN 315 Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 168 EYTTINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 361 tr <u>Q45848</u> Botulinum neurotoxin type B (Fragment) [BoNT/B] 361 Q45848 CLOBO [Clostridium AA botulinum] align Score = 298 bits (763), Expect = 2e-79 Identities = 144/166 (86%), Positives = 154/166 (92%) Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62 +KYLKTI+PFDLS YTN+ ILI++FNKYNSE RY+DNNLIDLSGYGAKVEVY Sbjct: 196 DKYLKTIIPFDLSTYTNNEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255 Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122 DGV+LNDKNQEKLTSSA+SKIRVTQNQNIIFMS+FLDFSVSFWIRIPKY+ND IQMYTHN Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN 315 Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 168 EYTTINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 361 sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295 BXA2 CLOBO (BoNT/A) AΑ (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align A light-chain; Botulinum neurotoxin A heavy-chain] [botA] [Clostridium botulinum] Score = 297 bits (761), Expect = 3e-79Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%) Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62 N L +PF LS Y ++ L+ F +Y YK ++LIDLS YGAK+ + Sbjct: 841 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 900 Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120 D V + DKNO KL + +S T V T++NS++ +FS SFWI+TPKY + + + Sbjct: 901 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 957 Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180 +NEYTIINC++NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FVT Sbjct: 958 NNEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWIFVT 1017 Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239 ITNN L +KIYING+L I ++ + A+ +I+FKLDG D ++I +KYF++F+ E

+KYLKTI+PFDLS+YTN+ ILI++FNKYNSE RY+DNNLIDLSGYGAKVEVY Sbjct: 196 DKYLKTIIPFDLSMYTNNEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255 Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122 DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYTHN Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN 315 Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 168 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 361 tr 045848 Botulinum neurotoxin type B (Fragment) [BoNT/B] 361 Q45848 CLOBO [Clostridium AΑ botulinum] <u>align</u> Score = 298 bits (763), Expect = 2e-79Identities = 144/166 (86%), Positives = 154/166 (92%) Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62 +KYLKTI+PFDLS YTN+ ILI++FNKYNSE RY+DNNLIDLSGYGAKVEVY Sbjct: 196 DKYLKTIIPFDLSTYTNNEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255 Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122 DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYTHN Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN 315 Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 168 EYTTINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED 361 sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295 BXA2 CLOBO (BoNT/A) AΑ (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align A light-chain; Botulinum neurotoxin A heavy-chain] [botA] [Clostridium botulinum] Score = 297 bits (761), Expect = 3e-79Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%) Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62 N L +PF LS Y ++ L+ F +Y YK ++LIDLS YGAK+ + Sbjct: 841 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 900 Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120 D V + DKNQ KL + +S I V I++NS++ +FS SFWI+TPKY + + + Sbjct: 901 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 957 Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180 +NEYTIINC++NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FVT Sbjct: 958 NNEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWIFVT 1017 Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239 ITNN L +KIYING+L I ++ + A+ +I+FKLDG D ++I +KYF++F+ E

tr <u>Q58GH1</u> Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA Q58GH1\_CLOBO

<u>align</u>

```
Score = 297 \text{ bits } (761), \text{ Expect} = 3e-79
 Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%)
N L +PF LS Y ++ L+ F +Y
                                               YK ++LIDLS YGAK+ +
Sbjct: 842 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 901
Query: 63
          DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
          D V + DKNQ KL + +s I V I++Ns++ +FS SFWI+IPKY + + +
Sbjct: 902 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 958
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           +MEYTIINC++NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FVT
Sbjct: 959 NNEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWIFVT 1018
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTE 239
           ITNN L +KIYING+L I ++ + A+ +I+FKLDG D ++I *KYF++F+ E
Sbjct: 1019 ITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1078
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
           L++ I++ Y QS S LKDEWGN L Y+K YYM N + N Y+ +
Sbjct: 1079 LNEKEIKDLYDSQSNSGILKDFWGNYLQYDKPYYMLNLFDPNKYVDVNNIGIRGYMYLKG 1138
Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
           P G ++T + Y ++ LY G KFII++ ++ D+IVR D +Y++
Sbjct: 1139 PRGSVVTTNIYLNST-----LYEGTKFIIKKYASGN--EDNIVRNNDRVYINVVVKNK 1189
Query: 351 EWRVYTXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIG 410
          E+R+ T
                             I D + +K D+Q + + +D D IG
Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRNKCKMNLQDNNGND-IG 1248
Query: 411 LIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
           IGH *
                   * S WY ++V + + GC+W+FIP D+GW E
```

```
Sbjct: 1018 ITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1077
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
           L++ I++ Y QS S LKDFWGN L Y+K YYM N + N Y+ +
Sbjct: 1078 LNEKEIKDLYDSQSNSGILKDFWGNYLQYDKPYYMLNLFDPNKYVDVNNIGIRGYMYLKG 1137
Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
           P G ++T + Y ++ LY G KFII++ ** D*IVR D *Y++
Sbjct: 1138 PRGSVVTTNIYLNST-----LYEGTKFIIKKYASGN--EDNIVRNNDRVYINVVVKNK 1188
Query: 351 EWRVYTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIG 410
                                       + +K D+Q + + +D D IG
           E+R+ T
                              T D
Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRNKCKMNLQDNNGND-IG 1247
Query: 411 LIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
           IG.E + + S WY ++V + +
                                               GC+W+FIP D+GW E
Sbjct: 1248 FIGFHLY-----DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1292
```

tr <u>Q58GH1</u> **Type A2 botulinum neurotoxin [Clostridium botulinum]** 1296 AA Q58GH1\_CLOBO

<u>align</u>

```
Score = 297 \text{ bits } (761), \text{ Expect} = 3e-79
 Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%)
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
Query: 3
           N L +PF LS Y ++ L+ F +Y
                                                  YK ++LIDLS YGAK+ +
Sbjct: 842 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 901
Query: 63
           DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
           D V + DKNQ KL + +S I V I++NS++ +FS SFWI+IPKY + + +
Sbjct: 902 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 958
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           +MEYTIINC++NNSGWK+S+ IIWTL D
                                             + \forall F+Y+
                                                       *IS+YINRW FVT
Sbjct: 959 NNEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWIFVT 1018
Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           ITNN L +KIYING+L I ++ + A+ +I+FKLDG D ++I *KYF++F+ E
Sbjct: 1019 ITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1078
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
           L++ I++ Y QS S LKDEWGN L Y+K YYM N + N Y+ +
Sbjct: 1079 LNEKEIKDLYDSQSNSGILKDFWGNYLQYDKPYYMLNLFDPNKYVDVNNIGIRGYMYLKG 1138
Query: 291 PVGEILTRSKYNONSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNO 350
           P G ++T + Y ++ LY G KFII++ ++ D+IVR D +Y++
Sbjct: 1139 PRGSVVTTNIYLNST-----LYEGTKFIIKKYASGN--EDNIVRNNDRVYINVVVKNK 1189
Query: 351 EWRVYTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIG 410
           医亚尼亚 中
                                I D
                                         + +K D+Q + + +D
Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRNKCKMNLQDNNGND-IG 1248
Query: 411 LIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
            IG H *
                        + S WY ++V + +
                                                  GC+W+FIF D+GW E
```

Sbjct: 1249 FIGFHLY-----DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1293

tr	<u>Q9ZAJ5</u> Q9ZAJ5		1280 AA align			
Score = 281 bits (720), Expect = 2e-74 Identities = 172/469 (36%), Positives = 255/469 (53%), Gaps = 35/469 (7%)						
Query	: 6	LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDG L + +PF+LS YTND ILI EN+ + RY++N ID+SGYG+ + +				
Sbjct	: 838	LNSSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGN				
Query	: 66	ELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN + ++NQF + S				
Sbjct:	: 898					
Query	: 124	YTIINCM-KNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFE YTTINCM NNSGWKIS*R R IIWTL D *G + + F Y IS*YIN*W E				
Sbjct:	955	YTIINCMGNNNSGWKISLRTIRDCEIIWTLQDTSGNKEKLIFRYEELASISDYINKWIE				
Query	: 180	TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFN TITNN L N++1YING L				
Sbjct	: 1015	TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSDNILFKIVGCDDET-YVGIRYFKVFN				
Query	: 239	ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEI-I EL: ++ TE Y + LKD+WGN L+YNK+YY+FN K+ YI ++S + I	т 297			
Sbjct	: 1074	ELDKTEIETLYSNEPDPSILKDYWGNYLLYNKKYYLFNLLRKDKYITRNSGILNINC	QQ 1131			
Query	298	RSKYNQNSKYINYRDLYIGEKFIIRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYR S ++NY+ LY G + LIR+ + N D+ VRE D Y++ + E+R+5				
Sbjct	: 1132	RGVTGGISVFLNYK-LYEGVEVIIRKNAPIDISNTDNFVRKNDLAYINVVDHGVEYRLY				
Query	: 357	XXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIF S+ ++ I + +C + F+ ++ S IGL+G F				
Sbjct	: 1191	DISITKSEKIIKLIRTSNPNDSLGQIIVMDSIGNNCTMNFQNNDGSNIGLLGFF				
Query	: 417	FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 D S WY ++R GC W FI K+ GW E				
Sbjct	: 1245	SDDLVASSWYYNHIRRNTSSNGCFWSFISKEHGWKE 1280				
		BoNT/F (Neurotoxin type F) [bont/f] [Clostridium LOBO botulinum]	1278 AA align			
Score = 281 bits (718), Expect = 3e-74 Identities = 166/465 (35%), Positives = 254/465 (53%), Gaps = 30/465 (6%)						
Query	: 6	LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDO L +PF+LS YTND ILT FNK + RY++N TD+SGYG+ + +				
Sbjct	: 838	L TETES ITNO ID: FAK T KITTA IDESGIGATE TE LNNSIPFELSSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGI				
Query	: 66	ELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN + +*NQF + SS S++ + QN +II+N + +FS+SFW+RIPKY N + ++2				

Sbjct: 1249 FIGFHLY------DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1293

tr	Q9ZAJ5 Q9ZAJ5	BonT protein [bonT] [Clostridium _ CLOBO botulinum]	1280 AA align	
		31 bits (720), Expect = 2e-74 = 172/469 (36%), Positives = 255/469 (53%), Gaps = 35/469	(7%)	
Query	7: 6	LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYD		
Sbjct	: 838	LNSSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISING		
Query	7: 66	ELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHI + ++NQE + S S++ + QN +II+NS + +FS+SFW+ IPK+ +N	NE 123 £	
Sbjct	: 898	YIYSTNRNQFGIYSGRLSEVNIAQNNDIIYNSRYQNFSISFWVTIPKHYRPMNRN		
Query	7: 124	YTIINCM-KNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF		
Sbjct	: 955	YTIINCMGNNNSGWKISLRTIRDCEIIWTLQDTSGNKEKLIFRYEELASISDYINKWI		
Query	7: 180	TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFT		
Sbjct	: 1015	TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSDNILFKIVGCDDET-YVGIRYFKVF		
Query	7: 239	ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEI-	LT 297	
Sbjct	: 1074	ELDKTEIETLYSNEPDPSILKDYWGNYLLYNKKYYLFNLLRKDKYITRNSGILNIN	QQ 1131 ·	
Query	7: 298	RSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRV R S ++NY+ LY G + LIR+ + N D+ VRK D Y++ + E+R+		
Sbjct	: 1132	RGVTGGISVFLNYK-LYEGVEVIIRKNAPIDISNTDNFVRKNDLAYINVVDHGVEYRL		
Query	7: 357	XXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGI S+ ++ I + +C + F+ ++ S IGE+G		
Sbjct	: 1191	DISITKSEKIIKLIRTSNPNDSLGQIIVMDSIGNNCTMNFQNNDGSNIGLLGF		
Query	y: 417	FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 D S WY ++R GC W FI K+ GW E		
Sbjct	: 1245	SDDLVASSWYYNHIRRNTSSNGCFWSFISKEHGWKE 1280		
		BoNT/F (Neurotoxin type F) [bont/f] [Clostridium LOBO botulinum]	1278 AA <u>align</u>	
Score = 281 bits (718), Expect = 3e-74 Identities = 166/465 (35%), Positives = 254/465 (53%), Gaps = 30/465 (6%)				
Query	y: 6	LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYD L +PF+LS YTND ILT FNK + RY++N ID+SGYG+ + +		
Sbjct	: 838	LNNSIPFELSSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISING	-	
Query	y: 66	ELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH + +*NQF + SS S++ + QN +II+N + +FS*SFW+RIPKY N + ++		

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Sbjct: 898 YIYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNE 954
Query: 124 YTIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTII+C++NN SGWKIS+ N+IIWTL D G + + F Y
                                                      IS+YIN+W FVTIT
Sbjct: 955 YTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTIT 1014
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
           NN L N++IYING L I ++ +* + I+FK+ G D T+++ ++YF +F+TEL
Sbjct: 1015 NNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELG 1073
Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
           ++ TE Y + LKDFWGN L+YNK YY+ N + T + + +
Sbjct: 1074 KTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSI-TQNSNFLNINQQRGVY 1132
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTXXXX 360
            + + + N R LY G + XIR+ ++ N D+ VRE D Y++ + + E+R+Y
Sbjct: 1133 QKPNIFSNTR-LYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISI 1191
Query: 361 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYES 420
                      S+S+ I + + +C + F+ + + IGL+G H
Sbjct: 1192 AKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH---- 1241
Query: 421 GIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWOFIPKDEGWTE 465
                       S WY
                             ++++ GC M EI K+ GM E
Sbjct: 1242 -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQE 1277
sp P30996
             Botulinum neurotoxin type F precursor (EC 3.4.24.69)
                                                                     1274
   BXF CLOBO (BoNT/F)
                                                                     AA
             (Bontoxilysin F) [botF] [Clostridium botulinum]
                                                                     align
 Score = 278 bits (712), Expect = 1e-73
 Identities = 171/474 (36%), Positives = 255/474 (53%), Gaps = 50/474 (10%)
         LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65
Query: 6
           L + +PF+LS YTND ILI FN+ +
                                             RY++N ID+SGYG+ + + V
Sbjct: 837 LNSSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNV 896
Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
               ++NQF + +S S*+ + QN *II+NS + +FS+SFW*RIPK+ N
Sbjct: 897 YIYSTNRNQFGIYNSRLSEVNIAQNNDIIYNSRYQNFSISFWVRIPKHYKPMNHN---RE 953
Query: 124 YTIINCM-KNNSGWKISIRGNR---IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179
           TTIINCM NNSGWKIS+P R IIWTL D +G +++ F Y IS YIN+W FV
Sbjct: 954 YTIINCMGNNNSGWKISLRTVRDCEIIWTLQDTSGNKENLIFRYEELNRISNYINKWIFV 1013
Query: 180 TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
           Sbjct: 1014 TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSDNILFKIVGCDDET-YVGIRYFKVFNT 1072
Query: 239 ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTR 298
           EL ++ IE Y + LK++WGN L+YNK+YY+FN
                                                 K+ YI L +S + I +
Sbjct: 1073 ELDKTEIETLYSNEPDPSILKNYWGNYLLYNKKYYLFNLLRKDKYITL--NSGILNINQQ 1130
```

Query: 299 SKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 357

+ S ++NY+ LY G + LIR+ N D+ VRK D Y++ + E+R+Y

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Sbjct: 898 YIYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNE 954
Query: 124 YTIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTII+C++NN SGWKIS+ N+IIWTL D G + + F Y
                                                       IS+YIN+W FVTIT
Sbjct: 955 YTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTIT 1014
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
           NN L N++IYING L I ++ +* + I+FK+ G D T+++ ++YF +F+TEL
Sbjct: 1015 NNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELG 1073
Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
           ++ IE Y + LKDFWGN L+YNK YY+ N + I + + + R Y
Sbjct: 1074 KTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSI-TQNSNFLNINQQRGVY 1132
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTXXXX 360
            + + + N R LY G + IIR+ ++ N D+ VRE D Y++ + + E+R+Y
Sbjct: 1133 QKPNIFSNTR-LYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISI 1191
Query: 361 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYES 420
                       S+S+ I + + +C + F+ + + IGL+G H
Sbjct: 1192 AKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH---- 1241
Query: 421 GIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                       S WY
                             ++++ GC W FI K+ GW E
Sbjct: 1242 -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQE 1277
sp P30996
                                                                       1274
             Botulinum neurotoxin type F precursor (EC 3.4.24.69)
   BXF CLOBO (BoNT/F)
                                                                       AΑ
             (Bontoxilysin F) [botF] [Clostridium botulinum]
                                                                       <u>align</u>
Score = 278 \text{ bits } (712), \text{ Expect = } 1e-73
Identities = 171/474 (36%), Positives = 255/474 (53%), Gaps = 50/474 (10%)
           LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65
Query: 6
           L + +PF+LS YTND ILI FN+ +
                                              RY++N ID+SGYG+ + + V
Sbjct: 837 LNSSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNV 896
Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
                ++NQF + +S S*+ + QN *II+NS + +FS+SFW*RIFK+ N
Sbjct: 897 YIYSTNRNQFGIYNSRLSEVNIAQNNDIIYNSRYQNFSISFWVRIPKHYKPMNHN---RE 953
Query: 124 YTIINCM-KNNSGWKISIRGNR---IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179
           YTTINCM NNSGWKIS+R R LIWTL D +G +++ F Y IS YIN+W EV
Sbjct: 954 YTIINCMGNNNSGWKISLRTVRDCEIIWTLQDTSGNKENLIFRYEELNRISNYINKWIFV 1013
Query: 180 TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
           TITNN L N++171MG L T ++ ++ + I+FK+ G D T ++ ++7F +FNT
Sbjct: 1014 TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSDNILFKIVGCDDET-YVGIRYFKVFNT 1072
Query: 239 ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTR 298
           EL ++ IE Y + LK++WGN L+YNK+YY+FN
                                                  K+ YI L +S + I +
Sbjct: 1073 ELDKTEIETLYSNEPDPSILKNYWGNYLLYNKKYYLFNLLRKDKYITL--NSGILNINQQ 1130
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Query: 299 SKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 357

+ S ++NY+ LY G + LIR+ N D+ VRK D Y+\* + E\*R+Y

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Query: 358 XXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTY-----SCQLLFKKDEESTDEIGL 411
                        S+++ T ++ Q
                                                +C + F+ + S
Sbjct: 1190 TK-----SEKEKIIRTSNLNDSLGQIIVMDSIGNNCTMNFQNNNGS--NIGL 1234
Query: 412 IGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
          +G H
                  + SWY ++R
                                             GC W I K+ GW E
Sbjct: 1235 LGFH-----SNNLVASSWYYNNIRRN--TSSNGCFWSSISKENGWKE 1274
sp Q00496
            Botulinum neurotoxin type E precursor (EC 3.4.24.69)
                                                                   1250
   BXE CLOBO (BoNT/E)
                                                                   AΑ
            (Bontoxilysin E) [Clostridium botulinum]
                                                                   align
Score = 273 \text{ bits } (699), \text{ Expect} = 4e-72
Identities = 163/469 (34%), Positives = 250/469 (52%), Gaps = 36/469 (7%)
          MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVE 60
              L +PF LS YT+D ILI ENK+
                                                BXK++ +D SGX + +
Sbjct: 813 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNIN 872
Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
          + 7
                  Sbjct: 873 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 931
Query: 119 YIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
           +*NEYTIINCM+ NNSGWK+S+ N IIWT D G + + F Y
Sbjct: 932 -VNNEYTIINCMRDNNSGWKVSLNHNEIIWTFEDNRGINQKLAFNYGNANGISDYINKWI 990
Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
          Sbjct: 991 FVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKIV-NCSYTRYIGIRYFNIF 1049
Query: 237 NTELSOSNIEERYKIOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEIL 296
          + EL ++ I+ Y + + LKDEWGN L+Y+KEYY+ N N++I +KDS
Sbjct: 1050 DKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDS----- 1103
Query: 297 TRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYT 356
          T S N S + LY G K I+B +NS S ND++VRE D +Y++F + + ++
Sbjct: 1104 TLSINNIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLFP 1160
Query: 357 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
                        IS S
                              +N + + +C + FK + + + IGL+G
Sbjct: 1161 LYADTATTNKEKTIKISSSGNRFNQVVVM----NSVGNCTMNFKNN--NGNNIGLLGFK- 1213
Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                          S WY + + + GC W FI ** GW E
Sbjct: 1214 -----ADTVVASTWYYTHM--RDHTNSNGCFWNFISEEHGWQE 1249
```

Sbjct: 1131 RGVTEGSVFLNYK-LYEGVEVIIRKNGPIDISNTDNFVRKNDLAYINVVDRGVEYRLYAD 1189

```
Sbjct: 1131 RGVTEGSVFLNYK-LYEGVEVIIRKNGPIDISNTDNFVRKNDLAYINVVDRGVEYRLYAD 1189
Query: 358 XXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTY-----SCQLLFKKDEESTDEIGL 411
                       S+ ++ T + + Q
                                               +C + F+ + S IGL
Sbjct: 1190 TK-----SEKEKIIRTSNLNDSLGQIIVMDSIGNNCTMNFQNNNGS--NIGL 1234
Query: 412 IGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                + SWY ++R GCW IK+GWE
Sbjct: 1235 LGFH------SNNLVASSWYYNNIRRN--TSSNGCFWSSISKENGWKE 1274
sp Q00496 Botulinum neurotoxin type E precursor (EC 3.4.24.69)
   BXE CLOBO (BONT/E)
                                                                  AA
            (Bontoxilysin E) [Clostridium botulinum]
                                                                  align
Score = 273 \text{ bits } (699), \text{ Expect} = 4e-72
Identities = 163/469 (34%), Positives = 250/469 (52%), Gaps = 36/469 (7%)
Query: 1 MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVE 60
          M L +PF LS YT+D TLI ENK+
                                               BXK++ +D SGX + +
Sbjct: 813 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNIN 872
Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
          + V +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N +
Sbjct: 873 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 931
Query: 119 YIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
           +*NEYTIINCM+ NNSGWK+S+ N IIWT D G + + F Y
Sbjct: 932 -VNNEYTIINCMRDNNSGWKVSLNHNEIIWTFEDNRGINQKLAFNYGNANGISDYINKWI 990
Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
          Sbjct: 991 FVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKIV-NCSYTRYIGIRYFNIF 1049
Query: 237 NTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEIL 296
          + EL ++ I+ Y + + LKDEWGN L+Y+KEYY+ N N++I +KDS
Sbjct: 1050 DKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDS----- 1103
Query: 297 TRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYT 356
          T S N S + LY G K I+B +NS S ND++VRK D +X++F + + ++
Sbjct: 1104 TLSINNIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLFP 1160
Query: 357 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
                        Sbjct: 1161 LYADTATTNKEKTIKISSSGNRFNQVVVM----NSVGNCTMNFKNN--NGNNIGLLGFK- 1213
Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                    D SWY + + + GCWFI ++ GWE
Sbjct: 1214 -----ADTVVASTWYYTHM--RDHTNSNGCFWNFISEEHGWQE 1249
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align

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Score = 267 bits (683), Expect = 3e-70
 Identities = 159/464 (34%), Positives = 247/464 (52%), Gaps = 36/464 (7%)
Query: 6
           LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDGV 65
           L +PE LS YT+D TLE FMK+
                                              RYK++ +D SGY + + +
Sbjct: 819 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGEI 878
Query: 66
           EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
               +KNQF + +S S++ ++QN II+++ + +FS+SFW+PIF Y N + I+NE
Sbjct: 879 FIYPTNKNQFTIFNSKPSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--INNE 936
Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTIINCM+ NNSGWK+S+ N IIWTL D + + F+Y
                                                      IS+YIN+W FVTIT
Sbjct: 937 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNARINQKLVFKYGNANGISDYINKWIFVTIT 996
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
           N+ L ++K+YING L I ++ + + I+FK+ + T++T ++YF+IF+ EL
Sbjct: 997 NDRLGDSKLYINGHLIDQKSILNLGNIHVSDNILFKIV-NCSYTRYIGIRYFNIFDKELD 1055
Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
           ++ I+ Y + + LKDFWGN L+Y+K YY+ N N++I +KDS
Sbjct: 1056 ETEIQTLYSNEPNTNILKDFWGNYLLYDKGYYLLNVLKPNNFIDRRKDS-----TLSIN 1109
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361
           N S + LYGK I+R N S ND VRK D +Y+++ + + + +Y
Sbjct: 1110 NIRSTILLANRLYSGIKVKIQR-VNDSSTNDRFVRKNDQVYINYISNSSSYSLYADTNTT 1168
Query: 362 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421
                  Sbjct: 1169 DKEKTIKSS--SSGNRFNQVVVMNSVGN----NCTMNFKNN--NGNNIGLLGFK----- 1214
Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                     S WY + + + GC W FI ++ GW E
                 D
Sbjct: 1215 -----ADTVVASTWYYTHM--RDHTNSNGCFWNFISEEHGWQE 1250
```

```
sp P30995 Botulinum neurotoxin type E precursor (EC 3.4.24.69)
BXE_CLOBU (BoNT/E)
(Bontoxilysin E) [Clostridium butyricum]

AA
align
```

```
Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 36/464 (7%)
Query: 6
           LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDGV 65
           L +PF LS YT+D ILI FNK+
                                               RYK++ +D SGY + + +
Sbjct: 818 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDV 877
Query: 66
           EL--NDKNOFKLTSSANSKIRVTONONIIFNSVFLDFSVSFWIRIPKYKNDGIONYIHNE 123
                +KNOE + +
                           S++ ++QN II+++ + +FS+SFW+RIP Y N + ++NE
Sbjct: 878 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 935
Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTTINCM+ MNSGWK+S+ N LIWTL D +G + + F Y
                                                        IS+YIN+W FVTIT
Sbjct: 936 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTIT 995
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
```

Score = 266 bits (680), Expect = 7e-70

```
Score = 267 \text{ bits } (683), \text{ Expect = } 3e-70
Identities = 159/464 (34%), Positives = 247/464 (52%), Gaps = 36/464 (7%)
           LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65
Query: 6
           L +PE LS YT+D ILI FNK+
                                              RXK++ +D SGX + + +
Sbjct: 819 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGEI 878
           EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
Query: 66
                +KNQF + +S S++ ++QN II+++ + +FS+SFW+RIF Y N + I+NE
Sbjct: 879 FIYPTNKNQFTIFNSKPSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--INNE 936
Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTIINCM+ NNSGWK+S+ N LIWTL D + + F+Y
                                                       IS+YIN+W FVTIT
Sbjct: 937 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNARINQKLVFKYGNANGISDYINKWIFVTIT 996
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
           N+ L ++K+YING L I ++ + + I+FK+ + T+FF EL
Sbjct: 997 NDRLGDSKLYINGHLIDQKSILNLGNIHVSDNILFKIV-NCSYTRYIGIRYFNIFDKELD 1055
Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
           ++ I+ Y + + LKDEWGN L+Y+K YY+ N N++I +KDS
Sbjct: 1056 ETEIQTLYSNEPNTNILKDFWGNYLLYDKGYYLLNVLKPNNFIDRRKDS-----TLSIN 1109
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361
           N S + LYGK I+R N S ND VRK D +Y+++ + + + +Y
Sbjct: 1110 NIRSTILLANRLYSGIKVKIQR-VNDSSTNDRFVRKNDQVYINYISNSSSYSLYADTNTT 1168
Query: 362 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421
                   + S + F
                             + + + +C + FK +
                                                    + + IGL+G
Sbjct: 1169 DKEKTIKSS--SSGNRFNQVVVMNSVGN----NCTMNFKNN--NGNNIGLLGFK----- 1214
Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                 D SWY + + + GCWFI++ GWE.
Sbjct: 1215 -----ADTVVASTWYYTHM--RDHTNSNGCFWNFISEEHGWQE 1250
sp P30995
             Botulinum neurotoxin type E precursor (EC 3.4.24.69)
                                                                       1250
   BXE CLOBU (BONT/E)
                                                                       AA
             (Bontoxilysin E) [Clostridium butyricum]
                                                                       align
Score = 266 \text{ bits } (680), \text{ Expect = } 7e-70
Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 36/464 (7%)
Query: 6
           LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDGV 65
           L +PF LS YT+D ILI + FNK+
                                               RYK++ +D SGY + + +
Sbjct: 818 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDV 877
Query: 66
           EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
                +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP X N + ++NE
Sbjct: 878 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 935
Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTIINCM+ NNSGWK+S+ N LIWIL D +G + + F Y IS+YIN+W FVTIT
Sbjct: 936 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTIT 995
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
```

tr <u>Q9FAR6</u> Type E botulinum toxin [bont/E] [Clostridium butyricum] 1255 AA Q9FAR6\_CLOBU

align

```
Score = 266 \text{ bits } (679), \text{ Expect = } 9e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%)
L +PF LS YT+D TLI FNK+
                                            RYK++ +D SGY + + + V
Sbjct: 822 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDV 881
Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
               +KNQF + + S++ ++QN TI+++ + +FS+SFW+RIF Y N + ++NE
Sbjct: 882 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 939
Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTIINCM+ NNSGWK+S+ N IIWTL D +G + + F Y IS+YIN+W FVTIT
Sbjct: 940 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTIT 999
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTELS 241
          N+ L ++K+YING L I ++ * + I+FK+ + T++I ++YF+IF+ EL
Sbjct: 1000 NDRLGDSKLYINGNLIDKKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELD 1058
Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
           ++ I+ Y + + LKDEWGN L+Y+KEYY+ N N++I + DS
Sbjct: 1059 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1112
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361
          N S + LY G K I+R +NS S ND++VRK D +Y++F + + +
Sbjct: 1113 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1169
Query: 362 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421
                    IS S
                         +N + + +C + FK + + + IGL+G
Sbjct: 1170 ATTNKEKTIKISSSGNRFNQVVVM---NSVGNNCTMNFKNN--NGNNIGLLGFK----- 1218
Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
```

```
Sbjct: 996 NDRLGDSKLYINGNLIDKKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELD 1054
Query: 242 QSNIEERYKIOSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
          ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS T S
Sbjct: 1055 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1108
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361
          N S + LY G K I+R +NS S ND++VRK D +Y++F + + +
Sbjct: 1109 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1165
Query: 362 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421
                        +N + * +C + FK + + + IGL+G
                   IS S
Sbjct: 1166 ATTNKEKTIKISSSGNRFNQVVVM----NSVGNCTMNFKNN--NGNNIGLLGFK----- 1213
Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                                  G W FI ++ GW E
                    SWX
                         4.4.
                               .
Sbjct: 1214 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1249
```

# tr <u>Q9FAR6</u> Type E botulinum toxin [bont/E] [Clostridium butyricum] 1255 AA Q9FAR6\_CLOBU

align

```
Score = 266 \text{ bits } (679), \text{ Expect = } 9e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%)
Query: 6 LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65
              +PF LS YT+D TLE FMK+
                                             RYK++ +D SGY + + + + V
Sbjct: 822 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDV 881
Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123
                +KNQF + + S++ ++QN II+++ + +PS+SFW+RIP Y N + ++NE
Sbjct: 882 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 939
Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
           YTIINCM+ NNSGWK+S+ N IIWTL D +G + + F Y IS+YIN+W FVTIT
Sbjct: 940 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTIT 999
Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
           Sbjct: 1000 NDRLGDSKLYINGNLIDKKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELD 1058
Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
           ++ I+ Y + + LKDEWGN L+Y+KEYY+ N N++I + DS T S
Sbjct: 1059 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1112
Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361
                    LY G K I+R +NS S MD++VRK D +Y++F + + +
Sbjct: 1113 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1169
Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421
                    IS S
                          +N++ +C+FK+++LGL+G
Sbjct: 1170 ATTNKEKTIKISSSGNRFNQVVVM---NSVGNNCTMNFKNN--NGNNIGLLGFK----- 1218
Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
```

D S WY ++ + G W ET ++ GW E
Sbjct: 1219 ----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1254

tr <u>Q8KZM3</u> Type E botulinum toxin [bont/E] [Clostridium butyricum] 1252 AA Q8KZM3 CLOBU align Score = 266 bits (679), Expect = 9e-70Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%) Query: 6 LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65 +PF LS YT+D ILI FNK+ RYK++ +D SGY + + + V Sbjct: 819 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDV 878 Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123 +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N + ++NE Sbjct: 879 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 936 Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182 YTTINCM+ NNSGWK+S+ N LIWTL D +G + + F Y IS+YIN+W FVTIT Sbjct: 937 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTIT 996 Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241 N+ T ++K+XIMC T I ++ + + I+EK+ + I++I ++XE+IE+ EP Sbjct: 997 NDRLGDSKLYINGNLIDKKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELD 1055 Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301 ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS T S Sbjct: 1056 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1109 Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361 N S \* LY G K I+R \*NS S ND++VRK D \*Y++F \* + + Sbjct: 1110 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1166 Query: 362 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421 IS S Sbjct: 1167 ATTNKEKTIKISSSGNRFNQVVVM---NSVGNNCTMNFKNN--NGNNIGLLGFK----- 1215 Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 S WY ++ + G W FI ++ GW E Sbjct: 1216 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1251

sp P19321 Botulinum neurotoxin type D precursor (EC 3.4.24.69) 1276
BXD\_CLOBO (Bont/D) AA

(Bontoxilysin D) [botD] [Clostridium botulinum] align

Score = 233 bits (594), Expect = 7e-60Identities = 160/484 (33%), Positives = 244/484 (50%), Gaps = 61/484 (12%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
N+ + MPF++ YTN+++L ++ N+Y + + K N L+D SGY A+V V
Sbjct: 833 NESFENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVG 892

D S WY ++ + G W ET ++ GW E Sbjct: 1219 ----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1254

tr Q8KZM3 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1252 AA Q8KZM3 CLOBU align Score = 266 bits (679), Expect = 9e-70Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%) Query: 6 LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65 L +PF LS YT+D ILI FNK+ RYK++ +D SGY + + + V Sbjct: 819 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDV 878 Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123 +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N + ++NE Sbjct: 879 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 936 Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182 TTTINCM+ NNSGWK+S+ N LIWTL D +G + + F Y IS+YIN+W FVTIT Sbjct: 937 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTIT 996 Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS 241  $p_{+} \in \mathbb{R} \ ++\mathsf{K}+\lambda \, \mathsf{IMG} \ \mathbb{R} \qquad \qquad \mathbb{R} \ ++ \ \ + \ \ \mathbb{R}+\lambda \, \mathsf{K}+ \qquad + + \lambda \, \mathsf{L}+\lambda \, \mathsf{$ Sbjct: 997 NDRLGDSKLYINGNLIDKKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELD 1055 Query: 242 QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301 ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS Sbjct: 1056 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1109 Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXXX 361 N S \* LY G K I+R +NS S ND++VRK D +Y++E \* + + Sbjct: 1110 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1166 Query: 362 XXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCOLLFKKDEESTDEIGLIGIHRFYESG 421 +N + + + + + TGL+G IS S Sbjct: 1167 ATTNKEKTIKISSSGNRFNQVVVM---NSVGNNCTMNFKNN--NGNNIGLLGFK----- 1215 Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465 D S WY ++ + G W FI ++ GW E Sbjct: 1216 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWOE 1251 sp F19321 Botulinum neurotoxin type D precursor (EC 3.4.24.69) 1276 BXD CLOBO (BoNT/D) AΑ (Bontoxilysin D) [botD] [Clostridium botulinum] align Score = 233 bits (594), Expect = 7e-60Identities = 160/484 (33%), Positives = 244/484 (50%), Gaps = 61/484 (12%) NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62 Query: 3 N+ + MPF++ YTN+++L ++ N+Y + + K N L+D SGY A+V V Sbjct: 833 NESFENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVG 892

Query:		DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI D V+LN N FKL+SS + KI V N NI++++++ + SVSFWI+I K +	
Sbjct:	893	DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS	946
Query:	121	HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT HNEYTIIN ++ NSGWK+ IR I W L D+N K ES+ F+Y+ + Y N+WFFVT	180
Sbjct:	947	HNEYTIINSIEQNSGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESLSHTGYTNKWFFVT	1006
Query:	181	ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE ITNN+ K+YTNG+L+ + I+D+ EV + T+F +D +TD O +W++ F+LF+ E	239
Sbjct:	1007	ITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE	1066
Query:	240	LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS LS +1 Y+ Q +KD+WGNPL ++ EYY+ N + YI +P +L	299
Sbjct:	1067	LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLVLV	1121
Query:	300	KYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXX +Y SK LY G I+ S+ + + D I I I ++++++	359
Sbjct:	1122	QYPDRSKLYTGNPITIKSVSDKNPYSRILNGDNIILHMLYNSRKYMI	1168
Query:	360	XXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR T D+D Y T Q E + Y+ +L + IG+ I	416
Sbjct:	1169		1212
Query:	417	FYESGIVFEE-YKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDE	461
Sbjct:	1213	KNKYCSQIFSSFRENTMLLADIYKPWRFSFKNAYTPVAVTNYETKLLSTSSFWKFISRDP	1272
Query:	462	GWTE 465	
Sbjct:	1273	GWVE 1276	
tr <u>0</u> 90		NTX (Fragment) [ntx] [Clostridium botulinum D	1275
Õaδ	TG/_C	BDP bacteriophage]	AA align
		31 bits (590), Expect = 2e-59 = 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (7%	<b>ታ</b> )
Query:	3	NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY N+ + MPF++ YTN+++L ++ N+Y + + K N L+D SGY A+V V	62
Sbjct:	833		892
Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI D V+LN N FKL+SS + KI V N NI++++++ * SVSFWI*I K +	120
Sbjct:	893	DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS	946
Query:	121	HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT	180

 $\texttt{ITNN+} \qquad \texttt{K+YING+L+} + \quad \texttt{I+D+} \; \texttt{EV} \quad + \quad \texttt{I+F} \; + \texttt{D} \; + \texttt{ID} \quad \texttt{Q} \; + \texttt{W++} \; \texttt{F+IF+} \; \texttt{E}$ 

Sbjct: 947 HNEYTIINSIEQNSGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESLSHTGYTNKWFFVT 1006

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239

Sbjct: 1007 ITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1066

Query:	63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI D V+LN N FKL+SS + KI V N NI++++++ + SVSFWI+I K +	120				
Sbjct:	893	DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS	946				
Query:	121	HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT ENEYTIIN ++ NSGWK+ IR T W L D+N K ES+ F+Y+ + Y N+WFFVT	180				
Sbjct:	947	HNEYTIINSIEQNSGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESLSHTGYTNKWFFVT	1006				
Query:	181	ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE ITNN+ K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+IF+ E	239				
Sbjct:	1007	ITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE	1066				
Query:	240	LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS LS +1 Y+ Q +KD+WGNPL ++ EYY+ N + YI +P +L	299				
Sbjct:	1067	LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLVLV	1121				
Query:	300	KYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXX +Y SK LY G I+ S* + * D I L +**+ +	359				
Sbjct:	1122	QYPDRSKLYTGNPITIKSVSDKNPYSRILNGDNIILHMLYNSRKYMI	1168				
Query:	360	XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR T D+D Y T Q E + Y+ +L + IG+ I	416				
Sbjct:	1169	IRDTDTIYAT-QGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVS	1212				
Query:	417	FYESGIVFEE-YKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDE F E+ ++ + YK + K V Y KL W+FT +D	461				
Sbjct:	1213	KNKYCSQIFSSFRENTMLLADIYKPWRFSFKNAYTPVAVTNYETKLLSTSSFWKFISRDP	1272				
Query:	462	GWTE 465					
Sbjct:	1273	GWVE 1276					
	1						
		NTX (Fragment) [ntx] [Clostridium botulinum D BDP bacteriophage]	1275 AA				
5.5	10,_0	DDI Dacteropage;	align				
Score							
Score = 231 bits (590), Expect = 2e-59  Identities = 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (7%)							
		31 bits (590), Expect = 2e-59 = 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (7%	;)				
Query:	ities	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX					
_	ities 3	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78	62				
_	3 833	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	62 892				
Sbjct: Query:	3 833 63	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78)  NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	62 892 120				
Sbjct: Query:	3 833 63 893	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78)  NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY  N+ + MPF++ YTN+++L ++ N+Y + + K N L+D SGY A+V V  NESFENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVG  DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI  D V+LN N FKL+SS + KI V N NI+++++ * SVSFWI+I K +  DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS  HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT	62 892 120 946				
Sbjct: Query: Sbjct: Query:	3 833 63 893 121	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78%)  NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	62 892 120 946 180				
Sbjct: Query: Sbjct: Query: Sbjct:	3 833 63 893 121 947	= 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (78)  NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY N+ + MPF++ YTN+++L ++ N+Y + + K N L+D SGY A+V V NESFENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVG  DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI D V+LN N FKL+SS + KI V N NI++++++ * SVSFWI+I K + DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT HNEYTIIN +* NSGWK+ IR I W L D+N K KS+ F+Y+ + Y N+WFFVT	62 892 120 946 180 1006				

```
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
                  Y+ Q +KD+WGNPL ++ EYY+ N + YI +P
           LS +T
Sbjct: 1067 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APESNVLVLV 1121
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333
                             I+ S+ S+ +N D
                       LY G
Sbjct: 1122 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1153
tr Q5DW55
                Type C botulinaum neurotoxin [bont/C] [Clostridium
                                                                      1280
   Q5DW55_CLOBO botulinum]
                                                                      AA
                                                                      <u>align</u>
 Score = 230 \text{ bits } (586), Expect = 6e-59
 Identities = 153/469 (32%), Positives = 240/469 (50%), Gaps = 31/469 (6%)
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
Query: 3
           N+ + +PF++ YTN+++L ++ N+Y +
                                                 + K N L+D SGY A+V *
Sbjct: 837 NESFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
Query: 63
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
                   N FKL+SS + KI V N NI+++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           ITMN+ K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+IF+ E
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLDEVKLDKTIVFGIDENIDENOMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
           LS +I Y+ Q +KD+WGNPL ++ EYYM N + YI
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYMINYNYIDRYI----APKNNILVLV 1125
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTXX 358
           +Y+ SK + I K + S+ +N DDI+ Y ++ +
Sbjct: 1126 QYSDISKLYTKNPITI--KSAANKNPYSRILNGDDIMFHMLYDSREYMIIRDTDTIYATQ 1183
Query: 359 XXXXXXXXXAPISDSDEFY--NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
                       + + + X IK \bigcirc X \subseteq +E ++L + \Gamma \Gamma++
Sbjct: 1184 GGQCSKNCVYALKLQSNLGNYGIGIFSIKNIVSQNKY-CSQIFSSFMKNT--MLLADIYK 1240
Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                 EE ++ + K + + M+EI +D CM E
Sbjct: 1241 PWR--FSFENAYTPVAVTNYETKLLSTSSF-----WKFISRDPGWVE 1280
               Type C botulinaum neurotoxin [bont/C] [Clostridium
                                                                      1280
   Q9LBS7_CLOBO botulinum]
                                                                      AΑ
                                                                      align
Score = 228 \text{ bits } (580), \text{ Expect = } 3e-58
Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)
```

```
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
                  A+ O +KD+MCMAF ++ EAA+ N + XI +5 +F
           LS +T
Sbjct: 1067 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APESNVLVLV 1121
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333
                     LY G I+ S+ S+ +N D
                SK
Sbjct: 1122 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1153
tr Q5DW55
                Type C botulinaum neurotoxin [bont/C] [Clostridium
   Q5DW55 CLOBO botulinum]
                                                                      AA
                                                                      align
 Score = 230 bits (586), Expect = 6e-59
 Identities = 153/469 (32%), Positives = 240/469 (50%), Gaps = 31/469 (6%)
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
           N+ + +PF++ YTN+++L ++ N+Y +
                                                + K N L+D SGY A+V +
Sbjct: 837 NESFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
Query: 63
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
                   N FKL+SS + KI V N NI++++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           ENEYTIIN +K MSGWK+ IR I W L DIN K KS+ F+Y+
                                                        + Y N+WEEVT
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           IINN+ K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+IF+ E
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
           LS +I
                  Y+ Q +KD+WGNPL ++ EYYM N + YI +P IL
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYMINYNYIDRYI----APKNNILVLV 1125
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTXX 358
           +Y+ SK + I K + S+ +N DDI+ Y ++ +
Sbjct: 1126 QYSDISKLYTKNPITI--KSAANKNPYSRILNGDDIMFHMLYDSREYMIIRDTDTIYATQ 1183
Query: 359 XXXXXXXXXAPISDSDEFY--NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
                       + + Y IK Q Y C +F ++T + L I++
Sbjct: 1184 GGQCSKNCVYALKLQSNLGNYGIGIFSIKNIVSQNKY-CSQIFSSFMKNT--MLLADIYK 1240
Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
                     W+FT +D GW E
                 FE
Sbjct: 1241 PWR--FSFENAYTPVAVTNYETKLLSTSSF-----WKFISRDPGWVE 1280
                                                                      1280
tr Q9LBS7
                Type C botulinaum neurotoxin [bont/C] [Clostridium
   Q9LBS7 CLOBO botulinum]
                                                                      AΑ
                                                                      <u>align</u>
 Score = 228 \text{ bits } (580), \text{ Expect = } 3e-58
 Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)
```

```
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
           N+ + +FF++ YTN+++L ++ N+Y +
                                                  + K N L+D SGY A+V +
Sbjct: 837 NESFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
Query: 63
            V++N N FKL+SS + KI V N MI++++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           ENEYTIIN +K NSGWE+ IR I W L DIN K KS+ F+Y+
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
                   K+YING+L+ + T+D+ EV + I+F +D +ID Q +W++ F+IF+ E
           TTNN+
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
           LS +I Y+ Q *KD+WGNPL ++ EYY+ N + YI +P IL
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APKSNILVLV 1125
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333
                SK
                      LY G I * S+ S+ +N D
Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157
     Q45849
tr
                          Neurotoxin [Clostridium botulinum C] 1280 AA
     Q45849 CLOBO
                                                                align
Score = 228 \text{ bits } (580), \text{ Expect} = 3e-58
Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
           N+ + +PF++ YTN+++L ++ N+Y + + K N L+D SGY A+V +
Sbjct: 837 NESFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
Query: 63
                   N FKL+SS + KI V N NI++++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           HMEYTIIN +K NSGWE+ IR I W L DIN K KS+ F+Y+ + Y N+WFFVT
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           TTNN+ K+YING+L+ + T+D+ EV + T+F +D +ID Q +W++ F+TF+ E
```

Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
LS +X X+Q +KD+WGNPL ++ EYY+ N + YX +P XL
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APKSNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333 +Y SK LY G I+ S+ S+ +N D Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

```
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
           N+ + +FF++ YTN+++L ++ N+Y +
                                                  + K N L+D SGY A+V +
Sbjct: 837 NESFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
Query: 63
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
             V++N N FKL+SS + KI V N MI+++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS----- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           HNEYTIIN +K NSGWK+ IR I W L DIN K KS+ F+Y+
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
                    K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+IF+ E
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
                    Y+ Q +KD+WGNPL ++ EYY+ N
                                                + YI
           LS +I
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APKSNILVLV 1125
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333
                       LY G I + S+ S+ +N D
           ÷Υ
                SK
Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157
tr
     Q45849
                         Neurotoxin [Clostridium botulinum C]
                                                                1280 AA
     Q45849 CLOBO
                                                                align
Score = 228 bits (580), Expect = 3e-58
Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
           N+ + +PF++ YTN+++L ++ N+Y + + K N L+D SGY A+V +
Sbjct: 837 NESFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
Query: 63
             V++N . N FKL+SS + KI V N NI++++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           HNEYTIIN +K NSGWK+ IR I W L DIN K KS+ F+Y+
                                                          + Y N+WFFVT
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           TTNN+ K+YING+L+ + T+D+ EV + I+F +D +ID Q +W++ F+TF+ E
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
           LS +I
                   X+ O +KD+MCNAT ++ EXX+ N
                                                + YI
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APKSNILVLV 1125
```

I+ S+ S+ +N D

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333

LY G Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

```
1280 AA
tr
     Q841S3
                           Neurotoxin [Clostridium botulinum]
     Q841S3_CLOBO
                                                                 align
 Score = 226 \text{ bits } (577), \text{ Expect = } 6e-58
 Identities = 131/338 (38%), Positives = 196/338 (57%), Gaps = 24/338 (7%)
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
Query: 3
           N + +PF++ YTN+++L ++ N+Y +
                                                   + K N L+D SGY A+V +
Sbjct: 837 NGSFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
Query: 63
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
                     N FKL+SS + KI V N NI+++++ + SVSFWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           HNEYTIIN +K NSGWK+ IR
                                   I W L DIN K KS+ F+Y+
                                                           + Y N+WFFVT
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
            ITNN+ K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+IF+ E
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
            LS +I
                  Y+ Q +KD+WGNPL ++ EYY+ N + YI
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APKSNILVLV 1125
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333
                SK LYG I+ S+
Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157
              Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylysin)
sp <u>P049</u>58
                                                                         1314
   TETX CLOTE [Contains:
                                                                         AΑ
              Tetanus toxin light chain (Tetanus toxin chain L);
                                                                         align
              Tetanus toxin heavy chain (Tetanus toxin chain H)] [tetX]
              [Clostridium tetani]
 Score = 211 \text{ bits } (538), Expect = 2e-53
 Identities = 137/434 (31%), Positives = 222/434 (50%), Gaps = 27/434 (6%)
Query: 46
           DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +N++T D+SG+ + V Y +L
                                      N - K
                                            L ++ +S++ V + +I +N +F +F
Sbjct: 891 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 949
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNS----GWKISIRGNRIIWTLIDINGK 155
           +VSEW+R+PK
                         ++ Y NEY+II+ MK +S GW +S++GN +IWTL D G+
Sbjct: 950 TVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLKGNNLIWTLKDSAGE 1009
Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
            + + F ++ + + Y+ N+W F+TITN+ L++A +YING L + +I + + +
Sbjct: 1010 VRQITFR-DLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1068
Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273
                   + Q++ + F IF L+ IE+ Y
                                                     +L+DFWGNPL Y+ EYY
Sbjct: 1069 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 1128
```

```
1280 AA
tr
     Q841S3
                           Neurotoxin [Clostridium botulinum]
     Q841S3 CLOBO
                                                                align
 Score = 226 \text{ bits } (577), \text{ Expect = } 6e-58
 Identities = 131/338 (38%), Positives = 196/338 (57%), Gaps = 24/338 (7%)
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
           N + +PF++ YTN+++L ++ N+Y +
                                                  + K N L+D SGY A+V +
Sbjct: 837 NGSFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRLE 896
           DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
Query: 63
                     N FKL+SS + KI V N NI++++++ + SVSEWI+I K
Sbjct: 897 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
           HNEYTIIN +K NSGWK+ IR I W L DIN K KS+ F+Y+
                                                          * A N#MAEAA
Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010
Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
           ITNN+ K+YING*L+ + I*D+ EV + I+F *D +ID Q +W++ F*IF+ E
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
           LS +I Y+ Q +KD+WGNPL ++ EYY+ N + YI +P IL
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYI----APKSNILVLV 1125
Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN----SQSINDD 333
           +Y SK LYG I+ S+ S+ +N D
Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157
              Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylysin)
                                                                        1314
sp P04958
   TETX CLOTE [Contains:
                                                                        AA
                                                                        align
              Tetanus toxin light chain (Tetanus toxin chain L);
              Tetanus toxin heavy chain (Tetanus toxin chain H)] [tetX]
              [Clostridium tetani]
 Score = 211 bits (538), Expect = 2e-53
 Identities = 137/434 (31%), Positives = 222/434 (50%), Gaps = 27/434 (6%)
Query: 46
           DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +N++T D+SG+ + V Y +L N K L ++ +S++ V + +T +N +F +F
Sbjct: 891 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 949
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNS----GWKISIRGNRIIWTLIDINGK 155
           +VSFW+R+PK ++ Y NEY+II+ MK +S
                                                GW +S++GN +IWTL D G+
Sbjct: 950 TVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLKGNNLIWTLKDSAGE 1009
Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
            * * F * + * + Y* N*W F*TITN+ L+*A *YING L + +I * + *
Sbjct: 1010 VRQITFR-DLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1068
```

Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273

Sbjct: 1069 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 1128

+ Q++ + F IF L+ IE+ Y +L+DFWGNPL Y+ EYY

I KLD

- tr Tetanus toxin (Fragment) [Clostridium Q9LA13 451 AA Q9LA13 CLOTE tetani] align Score = 211 bits (536), Expect = 4e-53Identities = 137/434 (31%), Positives = 220/434 (50%), Gaps = 27/434 (6%) Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNOFKLTSSANSKIRVTONONIIFNSVFLDF 100 +N++1 D+SG+ + V Y +L N E L ++ +S++ V + +1 +N +8 +F Sbjct: 28 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 86 Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKN----NSGWKISIRGNRIIWTLIDINGK 155 +VSFW+R+PK ++ Y NEY+II+ MK SGW +S++GN +IWTL D G+ Sbjct: 87 TVSFWLRVPKVSASHLEQYDTNEYSIISSMKKYSLSIGSGWSVSLKGNNLIWTLKDSAGE 146 Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213 Sbjct: 147 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 205 Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273 + Q++ + F IF L\* IE+ Y \*L+DEWGNPL Y+ EYY Sbjct: 206 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 265 Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333 + + ++LK + + Y I YR LY G KETI+R + + I D Sbjct: 266 LIPVAYSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYSGLKFIIKRYTPNNEI-DS 324 Query: 334 IVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390 VR D+I L NE V · + + Y ++ + + Sbjct: 325 FVRSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 384 Query: 391 PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450 TYS QL D++++ +GL+G H I + +D S WY Sbjct: 385 KTYSVQLKLYDDKDAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK----TL 435 Query: 451 GCNWQFIPKDEGWT 464 C+W F+P DEGWT Sbjct: 436 TCDWYFVPTDEGWT 449

Sbjct: 1299 GCDWYFVPTDEGWT 1312

- Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333 + + + + + + + + K + + Y I YR LY G KFII+R + + I D Sbjct: 1129 LIPVASSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYNGLKFIIKRYTPNNEI-DS 1187

  Query: 334 IVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390 V+ D+T L N E V + + Y ++ + + Y ++ + + Sbjct: 1188 FVKSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 1247

  Query: 391 PTYSCQLLFKKDEESTDEIGLIGHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450 TYS QL D+ ++ +GL+G H I + +D S WY +K K L Sbjct: 1248 KTYSVQLKLYDDKNAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK----IL 1298

  Query: 451 GCNWQFIPKDEGWT 464
  GC+W F+P DEGWT
- tr Q9LA13 Tetanus toxin (Fragment) [Clostridium 451 AA Q9LA13 CLOTE tetani] align Score = 211 bits (536), Expect = 4e-53Identities = 137/434 (31%), Positives = 220/434 (50%), Gaps = 27/434 (6%) Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100 +N++1 D+SG+ + V Y +L N K L ++ +S++ V + +1 +N +8 +F Sbjct: 28 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 86 Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKN----NSGWKISIRGNRIIWTLIDINGK 155 +VSFW+R+PK ++ Y NEY+II+ MK SGW +S++GN +1WTL D G+ Sbjct: 87 TVSFWLRVPKVSASHLEQYDTNEYSIISSMKKYSLSIGSGWSVSLKGNNLIWTLKDSAGE 146 Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213 + + F ++ + + Y+ N+W F+TITN+ L++A +YING L + +I + + + Sbjct: 147 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 205 Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273 + Q++ + F IF L+ IE+ Y +L+DEWGNPL Y+ EYY Sbjct: 206 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 265 Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333 + + ++LK + + Y I YR LY G KFIL+R + + I D Sbjct: 266 LIPVAYSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYSGLKFIIKRYTPNNEI-DS 324 Query: 334 IVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390 VR D+T L NE V Y ++ + + Sbjct: 325 FVRSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 384 Query: 391 PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450 TYS QL D++++ +GL+G H I + +D S WY +K K Sbjct: 385 KTYSVQLKLYDDKDAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK----TL 435 Query: 451 GCNWQFIPKDEGWT 464 C+W F+P DEGWT Sbjct: 436 TCDWYFVPTDEGWT 449

```
Neurotoxin consisting of botulinum neurotoxin D and C1
tr Q45967
   Q45967_CLOBO [Clostridium
                                                                   AΑ
                                                                   align
               botulinum D]
Score = 206 bits (523), Expect = 1e-51
Identities = 150/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)
Query: 3
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
          N+ + +PF++ YTN+++L +M N+Y + + K N L+D SGY A+V V
Sbjct: 833 NESFENTIPFNIFSYTNNSLLKDMINEYFNSINDSKILSLQNKKNTLMDTSGYNAEVRVE 892
Query: 63
          DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
           V+LN FKL SS + KT VTQN+NT++N+++ FS+SFWTRI K+ ++
Sbjct: 893 GNVQLNPIFPFDFKLGSSGDDRGKIIVTQNENIVYNAMYESFSISFWIRINKWVSN---- 948
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
               Sbjct: 949 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINFSYDISKNAAGY-NKWFF 1005
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
          VTIT N + N IYINGKL +K++ + + I F+++
Sbjct: 1006 VTITTNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
          W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYTNVVKDYWGNDLRYDKEYYMINVNYMNRYMSKKG 1124
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
               I + ++ N N D G K II+R + ND VR E+ +Y +
Sbjct: 1125 NG----IVFNTRKNNN------DFNEGYKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171
Query: 349 NQEWR--VYTXXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSCQLLFKKDEE 404
          Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230
Query: 405 STDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
          +T+ +G++ I + F+ DY+ ++ + +K + Y L +W F+P E
Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285
tr
     Q9LBR1
                         Neurotoxin [Clostridium botulinum] 1285 AA
     Q9LBR1 CLOBO
                                                          align
Score = 205 bits (522), Expect = 1e-51
Identities = 149/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)
Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
          N+ + +PF++ YTN+++L +M N+Y +
                                              + K N L+D SGY A+V V
Sbjct: 833 NESFENTIPFNIFSYTNNSLLKDMINEYFNSINDSKILSLQNKKNTLMDTSGYNAEVRVE 892
Query: 63
          DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
                     FKL SS +
                               K+ VTQN+NI++N+++ FS+SFWIRL K+ ++
Sbjct: 893 GNVQLNPIFPFDFKLGSSGDDRGKVIVTQNENIVYNAMYESFSISFWIRINKWVSN---- 948
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
```

```
tr Q45967
              Neurotoxin consisting of botulinum neurotoxin D and C1
   Q45967_CLOBO [Clostridium
                                                                    AA
                                                                    align
               botulinum D]
 Score = 206 bits (523), Expect = 1e-51
 Identities = 150/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)
Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
           N+ + +PF++ YTN+++L +M N+Y + + K N L+D SGY A+V V
Sbjct: 833 NESFENTIPFNIFSYTNNSLLKDMINEYFNSINDSKILSLQNKKNTLMDTSGYNAEVRVE 892
Query: 63
          DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
           V+LN FKL SS + KI VTON+NI++N+++ FS+SFWIRI K+ ++
Sbjct: 893 GNVQLNPIFPFDFKLGSSGDDRGKIIVTQNENIVYNAMYESFSISFWIRINKWVSN---- 948
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
               YTII+ +KNNSGW I I N +++TL + + F Y+I ++ + Y N+WFF
Sbjct: 949 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINFSYDISKNAAGY-NKWFF 1005
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD------GDIDRTQFI 228
           VTIT N + N IYINGKL +K++ + + I F+++
Sbjct: 1006 VTITTNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYTNVVKDYWGNDLRYDKEYYMINVNYMNRYMSKKG 1124
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
               I+ ++ N N D G K II+B + ND VR E+ +Y +
Sbjct: 1125 NG----IVFNTRKNNN------DFNEGYKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171
Query: 349 NQEWR--VYTXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSCQLLFKKDEE 404
           N+++ +Y A DE Y + II+ + Y+ Q LY
Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230
Query: 405 STDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
           Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285
tr
     Q9LBR1
                        Neurotoxin [Clostridium botulinum]
                                                            1285 AA
     Q9LBR1 CLOBO
                                                             align
Score = 205 bits (522), Expect = 1e-51
Identities = 149/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)
Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVY 62
          N+ + +PF++ YTN+++L +M N+Y + + K N L+D SGY A+V V
Sbjct: 833 NESFENTIPFNIFSYTNNSLLKDMINEYFNSINDSKILSLQNKKNTLMDTSGYNAEVRVE 892
Query: 63
          DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
                     FKL SS + K+ VTQN+NI++N+++ FS+SEWIRI K+ ++
Sbjct: 893 GNVQLNPIFPFDFKLGSSGDDRGKVIVTQNENIVYNAMYESFSISFWIRINKWVSN---- 948
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
```

```
XTII+ +KNNSGW I I N +++TL + + F X+I ++ + Y N+WEE
Sbjct: 949 -- LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINFSYDISKNAAGY-NKWFF 1005
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
           VTIT N + N IYINGKL +K++ + + I E+++
Sbjct: 1006 VTITTNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYTNVVKDYWGNDLRYDKEYYMINVNYMNRYMSKKG 1124
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
               I+ ++ N N D G K II+R + ND VR E+ +Y +
Sbjct: 1125 NG----IVFNTRKNNN------DFNEGYKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171
Query: 349 NQEWR--VYTXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSCQLLFKKDEE 404
           N+++ +Y A
                                    DE Y + I+ + Y+ O LY
Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230
Ouery: 405 STDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
           +T+ +G++ I + E+ DY+ ++ + +K + Y I_1 +W S+D E
Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285
    Q93N27
tr
                       Tetanus toxin (Fragment) [Clostridium
                                                                1310 AA
    Q93N27 CLOTE
                       tetani]
                                                                 align
 Score = 200 \text{ bits } (509), Expect = 5e-50
 Identities = 133/430 (30%), Positives = 216/430 (49%), Gaps = 27/430 (6%)
Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
          +N++I D+SG+ + V Y +L N K L ++ +S++ V + +I +N +F +F
Sbjct: 893 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 951
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKN-----NSGWKISIRGNRIIWTLIDINGK 155
           +VSEW+R+PK ++ Y NEY+II+ MK SGW +S++GN +IWTL D G+
Sbjct: 952 TVSFWLRVPKVSASHLEQYDTNEYSIISSMKKYSLSIGSGWSVSLKGNNLIWTLKDSAGE 1011
Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
           + + F ++ + + Y+ N+W F+TITN+ L++A +YING L + +I + + +
Sbjct: 1012 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1070
Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273
                  + Q++ + F IF L+ IE+ Y +L+DFWGNPL Y+ EYY
Sbjct: 1071 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 1130
Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333
           + + ++LK + + Y I YR LY G KFTT+R + + T D
Sbjct: 1131 LIPVAYSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYSGLKFIIKRYTPNNEI-DS 1189
Query: 334 IVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXXXPI---SDSDEFYNTIQIKEYDEQ 390
           VR D+I L N E V + + Y ++ + +
Sbjct: 1190 FVRSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 1249
Query: 391 PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
           TYS QL D++++ +GL+G H I + +D S WY +K K
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YTII+ +KNNSGW I I N +++Th + F Y+I ++ + Y N+WFF
Sbjct: 949 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINFSYDISKNAAGY-NKWFF 1005
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD------GDIDRTOFI 228
           VTIT N + N IYINGKL +K++ + + I E+++
Sbjct: 1006 VTITTNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYTNVVKDYWGNDLRYDKEYYMINVNYMNRYMSKKG 1124
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
               I+ ++ N N D G K II+R + ND VR E+ +Y +
Sbjct: 1125 NG----IVFNTRKNNN------DFNEGYKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171
Query: 349 NQEWR--VYTXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSCQLLFKKDEE 404
                               Α
                                     DE Y + T+ +
                                                        X+ O DE
Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230
Query: 405 STDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
           \pm T \pm \pm G \pm \pm I + \Sigma \pm DY \pm \pm \pm \pm \pm + K \pm Y = E \pm E
Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285
     Q93N27
tr
                        Tetanus toxin (Fragment) [Clostridium
                                                                 1310 AA
     Q93N27 CLOTE
                       tetani]
                                                                  align
 Score = 200 \text{ bits } (509), Expect = 5e-50
 Identities = 133/430 (30%), Positives = 216/430 (49%), Gaps = 27/430 (6%)
Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +N++T D+SG+ + V Y +L N K L ++ +S++ V + +T +N +F +P
Sbjct: 893 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 951
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKN-----NSGWKISIRGNRIIWTLIDINGK 155
           +VSEW+R+FK ++ Y NEY+II+ MK
                                              SGW +S++GN +IWTL D G+
Sbjct: 952 TVSFWLRVPKVSASHLEQYDTNEYSIISSMKKYSLSIGSGWSVSLKGNNLIWTLKDSAGE 1011
Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
           + + F ++ + + Y+ N+W F+TITN+ L++A +YING L + +I + + +
Sbjct: 1012 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1070
Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273
                   + Q++ + F IF L+ IE+ Y +L+DFWGNPL Y+ EYY
Sbjct: 1071 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 1130
Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333
           + + ++LK + + Y I YR LY G KFII+R + + I D
Sbjct: 1131 LIPVAYSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYSGLKFIIKRYTPNNEI-DS 1189
Query: 334 IVRKEDYIYLDFFNLNQEWRVYTXXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390
            VR D+I L NE V
                                             . 4 * Y ** 4 *
Sbjct: 1190 FVRSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 1249
Query: 391 PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
           TYS QL D++++ +GL+G H I + +D S WY +K K
```

Query: 451 GCNWQFIPKD 460

CHW F+P D

```
Sbjct: 1301 TCDWYFVPTD 1310
                                                                      1290
sp P18640
              Botulinum neurotoxin type C1 precursor (EC 3.4.24.69)
   BXC1 CLOBO (BoNT/C1)
                                                                      AΑ
              (Bontoxilysin C1) [Clostridium botulinum]
                                                                     align
 Score = 198 bits (503), Expect = 2e-49
 Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
           N + +PF++ YTN+++L ++ N+Y +
                                                + + N L+D SGY A+V
Sbjct: 836 NNSFQNTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEE 895
Query: 63
           DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
            V+LN FKL SS K+ VTQN+NI++NS++ FS+SFWIRI K+ ++
Sbjct: 896 GDVQLNPIFPFDFKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN---- 951
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
                YTII+ +KNNSGW I I N +++TL +S+ F Y+I + Y N+WFF
Sbjct: 952 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGY-NKWFF 1008
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD------GDIDRTOFI 228
           VT+TMN + N KIYINGKL +K++ + + I F+++
Sbjct: 1009 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1067.
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N
Sbjct: 1068 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRYMYANS 1127
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
               +I+ ++ N N D G K II+R + ND VR D +Y D
Sbjct: 1128 ----RQIVFNTRRNNN-----DFNEGYKIIIKRIRG--NTNDTRVRGGDILYFDMTIN 1174
Query: 349 NQEWRVY 355
           N+ + ++
Sbjct: 1175 NKAYNLF 1181
tr Q93HT3
               Type C botulinaum neurotoxin [bont/C] [Clostridium
                                                                     1291
   Q93HT3 CLOBO botulinum]
                                                                     AΑ
                                                                     align
Score = 198 bits (503), Expect = 2e-49
Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)
Query: 3
           NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
           + + N L+D SGY A+V
Sbjct: 837 NNSFQNTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEE 896
Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
```

Sbjct: 1250 KTYSVQLKLYDDKDAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK----TL 1300

Query: 451 GCNWQFIPKD 460

```
CHW F+P D
Sbjct: 1301 TCDWYFVPTD 1310
sp P18640
                                                                       1290
              Botulinum neurotoxin type C1 precursor (EC 3.4.24.69)
   BXC1 CLOBO (BoNT/C1)
                                                                       AΑ
              (Bontoxilysin C1) [Clostridium botulinum]
                                                                       align
 Score = 198 bits (503), Expect = 2e-49
 Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)
Query: 3
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
           N + +PF++ YTN+++L ++ N+Y +
                                                  + + N L+D SGY A+V
Sbjct: 836 NNSFQNTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEE 895
Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
            V+LN FKL SS K+ VTON+NI++NS++ FS+SFWIRI K+ ++
Sbjct: 896 GDVQLNPIFPFDFKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN---- 951
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
                YTII+ +KNNSGW I I N +++TL +S+ F Y+I + Y N+WFF
Sbjct: 952 -- LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGY-NKWFF 1008
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD------GDIDRTQFI 228
           VT+TNN + N KIYINGKL +K++ + I F+++
Sbjct: 1009 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1067
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N
Sbjct: 1068 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRYMYANS 1127
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
               +I+ ++ N N . D G K II+R + ND VR D +Y D
Sbjct: 1128 ----RQIVFNTRRNNN------DFNEGYKIIIKRIRG--NTNDTRVRGGDILYFDMTIN 1174
Query: 349 NQEWRVY 355
           N+ + ++
Sbjct: 1175 NKAYNLF 1181
tr Q93HT3
                                                                       1291
                Type C botulinaum neurotoxin [bont/C] [Clostridium
   Q93HT3 CLOBO botulinum]
                                                                       AΑ
                                                                       align
 Score = 198 \text{ bits } (503), \text{ Expect} = 2e-49
 Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)
Query: 3
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVY 62
           N + +PF++ XJN+++F ++ N+X +
                                                  + + N L+D SGY A+V
Sbjct: 837 NNSFQNTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEE 896
Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
```

Sbjct: 1250 KTYSVOLKLYDDKDAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK----TL 1300

```
V+LN FKL SS K+ VTQN+NI++NS++ FS+SFWIRI K+ ++
Sbjct: 897 GDVQLNPIFPFDFKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN---- 952
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
                YTTT+ +KNMSGW I I N +++TL +S+ F Y+T + Y N+WFF
Sbjct: 953 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGY-NKWFF 1009
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
           VT+TNN + N KIYINGKL +K++ + + I E+++
Sbjct: 1010 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1068
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N
Sbjct: 1069 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRYMYANS 1128
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
                +T+ ++ M N D G K TT+R + ND VR D +Y D
Sbjct: 1129 ----RQIVFNTRRNNN------DFNEGYKIIIKRIRG--NTNDTRVRGGDILYFDMTIN 1175
Query: 349 NQEWRVY 355
           N+ + ++
Sbjct: 1176 NKAYNLF 1182
tr Q7WUH9 Botulinum neurotoxin type B (Fragment) [bont/B]
                                                                          78 AA
   Q7WUH9 CLOBO [Clostridium
                botulinum]
                                                                          align
 Score = 148 \text{ bits } (374), \text{ Expect = } 2e-34
 Identities = 71/78 (91%), Positives = 74/78 (94%)
Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
          PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNONS YINYR*LYIGEKFIIRRK
Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIGEKFIIRRK 60
Query: 325 SNSQSINDDIVRKEDYIY 342
          SNSQSINDDIVR +D +Y
Sbjct: 61 SNSQSINDDIVRNDDRVY 78
tr Q7WRW0 Botulinum neurotoxin type B (Fragment) [bont/B]
                                                                         78 AA
   Q7WRW0 CLOBO [Clostridium
                botulinum]
                                                                          align
Score = 147 \text{ bits } (370), \text{ Expect} = 6e-34
Identities = 70/78 (89%), Positives = 74/78 (94%)
Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
          PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR+LYIGEKFIIRRK
Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIGEKFIIRRK 60
Query: 325 SNSQSINDDIVRKEDYIY 342
          SNSQSINDDIVR +D ++
Sbjct: 61 SNSQSINDDIVRNDDRVF 78
```

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V+LN FKL SS K+ VTQN+NI++MS++ FS+SFWIRL K+ ++
Sbjct: 897 GDVQLNPIFPFDFKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN---- 952
Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
                YTTI+ +ENNSGW I I N +++TL +S+ F Y+I + Y N+WFF
Sbjct: 953 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGY-NKWFF 1009
Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD------GDIDRTQFI 228
           VT+TNN + N KIYINGKL +K++ + + I F+++
Sbjct: 1010 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1068
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
           W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N
Sbjct: 1069 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRYMYANS 1128
Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
                +T+ ++ N N D G K TT+R + ND VR D +Y D
Sbjct: 1129 ----RQIVFNTRRNNN------DFNEGYKIIIKRIRG--NTNDTRVRGGDILYFDMTIN 1175
Query: 349 NQEWRVY 355
           N+ + ++
Sbjct: 1176 NKAYNLF 1182
tr Q7WUH9 Botulinum neurotoxin type B (Fragment) [bont/B]
                                                                          78 AA
   Q7WUH9 CLOBO [Clostridium
                botulinum]
                                                                          align
 Score = 148 \text{ bits } (374), \text{ Expect} = 2e-34
Identities = 71/78 (91%), Positives = 74/78 (94%)
Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
          PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTESKYNONS YINYR*LYIGEKFILERK
Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIGEKFIIRRK 60
Query: 325 SNSQSINDDIVRKEDYIY 342
          SNSQSINDDIVR +D +Y
Sbjct: 61 SNSQSINDDIVRNDDRVY 78
tr Q7WRW0 Botulinum neurotoxin type B (Fragment) [bont/B]
                                                                          78 AA
   Q7WRW0_CLOBO [Clostridium
                                                                          align
                botulinum]
 Score = 147 \text{ bits } (370), \text{ Expect = } 6e-34
Identities = 70/78 (89%), Positives = 74/78 (94%)
Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
          PLMYNKEYYMFNAGNKNSYIKLKKDS VGETLTRSKYNONS YINYR+LYIGEKFIIRRK
Sbjct: 1
          PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIGEKFIIRRK 60
Query: 325 SNSQSINDDIVRKEDYIY 342
          SNSQSINDDIVR +D ++
Sbjct: 61 SNSQSINDDIVRNDDRVF 78
```

Non-proteolytic neurotoxin type B (Fragment) [Clostridium 77 AA tr <u>Q6Q799</u> Q6Q799\_CLOBO botulinum] align Score = 146 bits (368), Expect = 1e-33 Identities = 71/77 (92%), Positives = 73/77 (94%) Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324 PLMYNKEYYMFNAGNKNSYIKL KDS VGEIL RSKYNQNS YINYR+LYIGEKFIIRR+ Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILIRSKYNQNSNYINYRNLYIGEKFIIRRE 60 Query: 325 SNSQSINDDIVRKEDYI 341 SNSQSINDDTVRKEDYT Sbjct: 61 SNSQSINDDIVRKEDYI 77 tr <u>Q</u>79AH9 Botulinum neurotoxin type F (Fragment) [BoNT/F] 366 Q79AH9 CLOBO [Clostridium AΑ botulinum] align Score = 142 bits (359), Expect = 1e-32Identities = 72/161 (44%), Positives = 104/161 (63%), Gaps = 6/161 (3%) LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65 +FF+LS YTND ILI FNK RY++N ID+SGYG+ + + V Sbjct: 204 LNNSIPFELSSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDV 263 Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123 ++NQF + SS S++ + QN +II+N + +FS+SFW+RIPKY N + ++NE Sbjct: 264 YIYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNE 320 Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163 YTTI+C++ NNSGWKIS+ N+IIWTL D G + + F Y Sbjct: 321 YTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNY 361 tr Q45861 367 Botulinum neurotoxin type E (Fragment) [BoNT/E] Q45861 CLOBO [Clostridium ΑA botulinum] <u>align</u> Score = 133 bits (335), Expect = 7e-30Identities = 68/166 (40%), Positives = 99/166 (58%), Gaps = 5/166 (3%) Query: 1 MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXKYKDNNLIDLSGYGAKVE 60 +PF LS YT+D ILI FNK+ RYK++ +D SGY + + Sbjct: 199 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNIN 258 Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118 +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N + Sbjct: 259 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 317 Query: 119 YIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163 ++NEYTIINCM+ NNSGWK+S+ N IIWTL D G + + F Y Sbjct: 318 -VNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNY 362

tr <u>Q6Q799</u> Non-proteolytic neurotoxin type B (Fragment) [Clostridium 77 AA Q6Q799 CLOBO botulinum align Score = 146 bits (368), Expect = 1e-33 Identities = 71/77 (92%), Positives = 73/77 (94%) Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324 PLMYNKEYYMFWAGNKNSYIKL KDS VGEIL RSKYNQNS YINYR+LYIGEKFILRR+ PLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILIRSKYNQNSNYINYRNLYIGEKFIIRRE 60 Query: 325 SNSQSINDDIVRKEDYI 341 SNSQSINDDIVRKEDYI Sbjct: 61 SNSQSINDDIVRKEDYI 77 tr Q79AH9 Botulinum neurotoxin type F (Fragment) [BoNT/F] 366 Q79AH9 CLOBO [Clostridium AΑ botulinum] <u>align</u> Score = 142 bits (359), Expect = 1e-32Identities = 72/161 (44%), Positives = 104/161 (63%), Gaps = 6/161 (3%) LKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV 65 \*PF+LS YTND ILI FNK \* RY++N ID+SGYG\* + + Sbjct: 204 LNNSIPFELSSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDV 263 Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123 ++NQF + SS S++ + QN +II+N + +FS+SFW+BIPKY N + ++NE Sbjct: 264 YIYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNE 320 Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163 YTTI+C++ NNSGWKIS+ N+LIWTL D G + + F Y Sbjct: 321 YTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNY 361 Botulinum neurotoxin type E (Fragment) [BoNT/E] tr Q45861 367 Q45861\_CLOBO [Clostridium AΑ botulinum] align Score = 133 bits (335), Expect = 7e-30Identities = 68/166 (40%), Positives = 99/166 (58%), Gaps = 5/166 (3%) Query: 1 MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXRYKDNNLIDLSGYGAKVE 60 +PF LS YT+D ILI FNK+ RYK++ +D SGY + + Sbjct: 199 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNIN 258 Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118 +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N + Sbjct: 259 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 317 Query: 119 YIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163 ++NEYTIINCM+ NNSGWK+S+ N IIWTL D G + + F Y Sbjct: 318 -VNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNY 362

tr	006018	NTNH protein [NTNH] [Clostridium CLOBO botulinum]	1198 AA <u>align</u>					
Score = 85.5 bits (210), Expect = 2e-15 Identities = 79/347 (22%), Positives = 145/347 (41%), Gaps = 63/347 (18%)								
Query	·: 51	DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRI D+SG V+ D ++L+ V + NI N + FS+ FW+R	PK 110					
Sbjct	: 853	DISGKDTLVQYSDTIDLSYGVNGDALYLKEPNQSVNFSNNIFENGLTNSFSICFWLR-	909					
Query	: 111	YKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED N G N N +I + NN GW+I N ++++++D NG K+++ + + +						
Sbjct	: 910							
Query	: 171	EYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ	FI 228					
Sbjct	: 961	KYWYYISVSVDRLRNKLLIFINDKLIVNESIEQILNIYSSNIISLVNENN	PI 1012					
Query	: 229	WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN	-A 277					
Sbjct	: 1013	CIEELSILNKALTSEEVLNSYFTNLNNSYIRDSYGARLEYNKNYELYNYVFPENSLYE	/I 1072					
Query	: 278	GNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGENN N Y+ +K + + + + + + + + + + + + + + + + +	KF 319					
Sbjct	: 1073	ENNNMYLSIKNIKNTNILGAKFKLINTDESKQYVQKWDEVIICVLGDTEKYADIQAGNI	NR 1132					
Query	: 320	IIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRV 354 I + K N++ I N++I R						
Sbjct	: 1133	IQLVNSKDNARKIIVNNNIFRPNCVLFSYNNKYLSLSLRNRNYNWMI 1179						
		•						
tr O	15000	Nontoxic-hemagglutinin [nontoxic-hemagglutinin]	1197					
		LOBO [Clostridium botulinum]	AA align					
Score = 77.4 bits (189), Expect = 6e-13 Identities = 83/386 (21%), Positives = 159/386 (40%), Gaps = 71/386 (18%)								
Query	: 16		2F 73					
Sbjct	: 819	+ T++T LI K E +DNN + D+SG V+ D + L LITSETDLIKEEKESDYNLFLLTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVI	NG 874					
Query	74							
Sbjct	: 875		⊦N ON 926					
Query	: 134		ΚΙ 190					
Sbjct	: 927	GW+I N +++++++D NG +++++ + S+ I++ W+++++I+ + N CGWEIYFENNGLVFSIVDCNGNEENIYLSDVISKNWYYISISIDRLRNQL	.i. LI 978					
Query	: 191	YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERY +IN KL +N I+ I +++ I +++ SI N +++ * * * * * * * * * * * * * * * * *						
Sbjct	: 979	FINDKLIANQSIEQILNIYSSSTISLVNENNPIYVEGLSILNRSITSEEVVNN						

tr		NTNH protein [NTNH] [Clostridium botulinum]	1198 AA align				
Score = 85.5 bits (210), Expect = 2e-15 Identities = 79/347 (22%), Positives = 145/347 (41%), Gaps = 63/347 (18%)							
Query	: 51	DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRI	PK 110				
Sbjct	: 853	D+SG V+ D++L+ V + NI N + FS+ FW+R DISGKDTLVQYSDTIDLSYGVNGDALYLKEPNQSVNFSNNIFENGLTNSFSICFWLR-	909				
Query	: 111	YKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRED					
Sbjct	: 910						
Query	: 171	EYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQI	FI 228				
Sbjct	: 961	KYWYYISVSVDRLRNKLLIFINDKLIVNESIEQILNIYSSNIISLVNENN	***				
Query	: 229	WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN	-A 277				
Sbjct	: 1013	CIEELSILNKALTSEEVLNSYFTNLNNSYIRDSYGARLEYNKNYELYNYVFPENSLYE	/I 1072				
Query	: 278	GNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEIN N N Y+ +K + + K +++ +Y+ Y D+ G	KF 319				
Sbjct	: 1073	ENNNMYLSIKNIKNTNILGAKFKLINTDESKQYVQKWDEVIICVLGDTEKYADIQAGNI	NR 1132				
Query	: 320	IIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRV 354 I + K N++ T N++T R Y+ L N N W +					
Sbjct	: 1133	IQLVNSKDNARKIIVNNNIFRPNCVLFSYNNKYLSLSLRNRNYNWMI 1179					
	<u>45888</u> 45888_C	Nontoxic-hemagglutinin [nontoxic-hemagglutinin]  LOBO [Clostridium botulinum]	1197 AA <u>align</u>				
Score = 77.4 bits (189), Expect = 6e-13 Identities = 83/386 (21%), Positives = 159/386 (40%), Gaps = 71/386 (18%)							
Query	: 16	IYTNDTILIEMFNKYNSEXXXXXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKNG + T++T LI K E +DNN + D+SG V+ D + L	QF 73				
Sbjct	: 819	LITSETDLIKEEKESDYNLFLLTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVI	NG 874				
Query	: 74		NN 133 ⊹N				
Sbjct	: 875		= :				
Query	: 134		KI 190				
Sbjct	: 927	CGWEIYFENNGLVFSIVDCNGNEENIYLSDVISKNWYYISISIDRLRNQL	•••				
Query	: 191	YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERY +IN KL +N I+ I + ++ I ++ I +++ SI N +++ *					
Sbjct	: 979	FINDKLIANQSIEQILNIYSSSTISLVNENNPIYVEGLSILNRSITSEEVVNN					

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Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN------AGNKNSYIKLKKDSPV---GEIL 296
+ Y++D G L YNK Y ++N N N Y+ *K + + G
Sbjct: 1034 SYLNNSYIRDISGERLEYNKIYELYNYVFPENSLYEVTENNNIYLSIKDTNDLNIQGAKF 1093
Query: 297 TRSKYNQNSKYINYRD-----LYIGEKFIIRRKSNSQ------SINDDIVR- 336
                + N +Y+ D L EK++ N++
                                                            N+DI +
Sbjct: 1094 KLINIDTNKQYVQKWDEGVVCLLGDEEKYVDISSENNRIQLVSSRDTAKKIIFNNDIFKP 1153
Query: 337 -----KEDYIYLDFFNLNQEWRVY 355
                    X \leftarrow Y Y Y Y Y Y
Sbjct: 1154 NCLTFAYNNKYLSLSFRDRNYNWMIY 1179
sp P46082 Botulinum neurotoxin type E, nontoxic component [ent-120] 1162 AA
   BXEN_CLOBO [Clostridium botulinum]
                                                                     align
 Score = 74.7 bits (182), Expect = 4e-12
 Identities = 70/286 (24%), Positives = 129/286 (44%), Gaps = 39/286 (13%)
Query: 45 KDNNLI-DLSGYGAKVEVYDGVELN---DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +DNN+I D SG VE + L + N LT AN I+ T + N + +F
Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHLTG-ANQNIKFTNDY--FENGLTNNF 866
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
           S+ FW+B K QN I ++ +I ++N GW+I + +++ +ID NG K+++
Sbjct: 867 SIYFWLRNLK-----QNTIKSK--LIGSKEDNCGWEIYFENDGLVFNIIDSNGNEKNIY 918
Query: 161 FEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
                 +IS + ++T + I+I+ L +N DIK+I + ++ I
Sbjct: 919 L----SNISNKSWHYIVISINRLKDQLLIFIDNILVANEDIKEILNIYSSDIISLLSDN 973
Query: 221 DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN---- 276
           + ++++ S+N ++ + T Y + Y+++P T YN+ Y+PN
Sbjct: 974 N----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFNYVFP 1028
Query: 277 -----AGNKNSYIKLKKDSPVGEILTRSKY---NQNSKYINYRD 312
                   NNY++++++ KNNN+Y+ D
Sbjct: 1029 EIAINKIEQNNNIYLSINNENNLNFKPLKFKLLNTNPNKQYVQKWD 1074
                       NTNHA [ntnha] [Clostridium botulinum] 1196 AA
tr
     Q9LBS8
     Q9LBS8 CLOBO
                                                              align
Score = 74.7 bits (182), Expect = 4e-12
Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)
Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
           R + N + I D + SG + + + VEL + SN + + N N + +
Sbjct: 843 RGPNSNIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900
Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
           F++ FW+R K+D I N+ NN GW+I N +++ +ID NG +SV
Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952
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Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN------AGNKNSYIKLKKDSPV---GEIL 296
+ Y++D G L YNK Y ++N N N Y+ *K ++ G
Sbjct: 1034 SYLNNSYIRDISGERLEYNKIYELYNYVFPENSLYEVTENNNIYLSIKDTNDLNIQGAKF 1093
Query: 297 TRSKYNQNSKYINYRD-----LYIGEKFIIRRKSNSQ-----SINDDIVR- 336
                + N +Y+ D E EK++ N++
                                                            M+DT+
Sbjct: 1094 KLINIDTNKQYVQKWDEGVVCLLGDEEKYVDISSENNRIQLVSSRDTAKKIIFNNDIFKP 1153
Query: 337 -----KEDYIYLDFFNLNQEWRVY 355
                    Y+I; F+N; W+Y
Sbjct: 1154 NCLTFAYNNKYLSLSFRDRNYNWMIY 1179
sp P46082 Botulinum neurotoxin type E, nontoxic component [ent-120] 1162 AA
   BXEN_CLOBO [Clostridium botulinum]
                                                                     align
 Score = 74.7 bits (182), Expect = 4e-12
 Identities = 70/286 (24%), Positives = 129/286 (44%), Gaps = 39/286 (13%)
Query: 45 KDNNLI-DLSGYGAKVEVYDGVELN---DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +DNN+I D SG VE + L + N LT AN I+ T + N + +F
Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHLTG-ANQNIKFTNDY--FENGLTNNF 866
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160 ·
           S+ FW+B K QN I ++ +I ++N GW+I + +++ +ID NG K+++
Sbjct: 867 SIYFWLRNLK-----QNTIKSK--LIGSKEDNCGWEIYFENDGLVFNIIDSNGNEKNIY 918
Query: 161 FEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
                 +IS + ++T + I+I+ L +N DIK+T + ++ I D
Sbjct: 919 L----SNISNKSWHYIVISINRLKDQLLIFIDNILVANEDIKEILNIYSSDIISLLSDN 973
Query: 221 DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN---- 276
           + ++++ S+ N ++ + T Y + Y++F L YN+ Y +FN
Sbjct: 974 N----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFNYVFP 1028
Query: 277 -----AGNKNSYIKLKKDSPVGEILTRSKY---NQNSKYINYRD 312
                   N N Y + + + + + + K N N + Y + D
Sbjct: 1029 EIAINKIEQNNNIYLSINNENNLNFKPLKFKLLNTNPNKQYVQKWD 1074
                         NTNHA [ntnha] [Clostridium botulinum] 1196 AA
t.r
     Q9LBS8
     Q9LBS8 CLOBO
                                                              align
 Score = 74.7 bits (182), Expect = 4e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)
Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
           R ++N+I D+SG ++ + VEL
                                     + SN + + N N + +
Sbjct: 843 RGPNSNIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900
Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
           F++ FW+R K+D I N+ NN GW+I N +++ +ID NG +SV
Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952
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Query: 160 FFEYNIREDISEYINRWFFVTIT--NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
              I N W++++I* + + I+IN K +N I+ I + + I
Sbjct: 953 YLSNVIN-----NNWYYISISVDRSKDQLLIFINDKNVANVSIEQILNIYSTNVISL- 1004
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
              +++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N
Sbjct: 1005 ----VNKNNSIYVEELSVLDKTVTSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNY 1060
Query: 277 -----AGNKNSYIKLK 287
                      N 87+ EK
Sbjct: 1061 VFPKTSLYEVNDNNKSYLSLK 1081
sp Q06366 Botulinum neurotoxin type E, nontoxic component
                                                                     1162
   BXEN CLOBU [Clostridium
                                                                    AA
             butyricum]
                                                                    <u>align</u>
 Score = 74.3 bits (181), Expect = 5e-12
Identities = 62/236 (26%), Positives = 112/236 (47%), Gaps = 25/236 (10%)
Query: 45 KDNNLI-DLSGYGAKVEVYDGVELN---DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +DNN+I D SG VE + L + N LT AN I+ T + N + +F
Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHLTG-ANQNIKFTNDY--FENGLTNNF 866
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
           S+ FW+R QN I ++ +I ++N GW+I N +++ +ID NG K+++
Sbjct: 867 SIYFWLRNLN-----QNTIKSK--LIGSKEDNCGWEIYFENNGLVFNIIDSNGNEKNIY 918
Query: 161 FEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
                 +1S + ++1 + 1+1+ L +N DIK+1 + ++ 1
Sbjct: 919 L----SNISNKSWHYIVISINRLKDQLLIFIDNILVANEDIKEILNIYSSDIISLLSDN 973
Query: 221 DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN 276
               ++++ S+N ++ + T Y + Y+++F L YN+ Y +FN
Sbjct: 974 N----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFN 1024
                                                                1197 AA
tr
     Q9ZAJ9
                        Ntnh protein [ntnh] [Clostridium
     Q9ZAJ9 CLOBO
                       botulinum]
                                                                 align
Score = 74.3 bits (181), Expect = 5e-12
Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)
Query: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
           + T++T LI
                     K E
                                     +DNN + D+SG
                                                   V+ D + L
Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
                     V+ + N + FS+ FW+R N G ++ I ++ +I
Sbjct: 875 DALYLKEPDESVSFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926
Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
           GW+I N ++++++D NG ++++ +S+ I++ W++++I+ + N I
Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNOLLI 978
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Query: 160 FFEYNIREDISEYINRWFFVTIT--NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
           + I N W++++I+ + + I+IN K +N I+ I + + I
Sbjct: 953 YLSNVIN-----NNWYYISISVDRSKDQLLIFINDKNVANVSIEQILNIYSTNVISL- 1004
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
              +++ I+++ S+ + ++ + Y + Y++D + L YNE Y ++N
Sbjct: 1005 ----VNKNNSIYVEELSVLDKTVTSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNY 1060
Query: 277 -----AGNKNSYIKLK 287
                     N SY+ LK
Sbjct: 1061 VFPKTSLYEVNDNNKSYLSLK 1081
sp Q06366 Botulinum neurotoxin type E, nontoxic component
                                                                    1162
   BXEN CLOBU [Clostridium
                                                                    AΑ
             butyricum]
                                                                    align
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 62/236 (26%), Positives = 112/236 (47%), Gaps = 25/236 (10%)
Query: 45 KDNNLI-DLSGYGAKVEVYDGVELN---DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
           +DNN+I D SG VE + L + N LT AN I+ T + N + +F
Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHLTG-ANQNIKFTNDY--FENGLTNNF 866
Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
           S+ FW+R QN I ++ +I ++N GW+I N +++ +ID NG K+++
Sbjct: 867 SIYFWLRNLN-----QNTIKSK--LIGSKEDNCGWEIYFENNGLVFNIIDSNGNEKNIY 918
Query: 161 FEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
                +IS + ++I + I+I+ L +N DIK+I + ++ I D
Sbjct: 919 L----SNISNKSWHYIVISINRLKDQLLIFIDNILVANEDIKEILNIYSSDIISLLSDN 973
Query: 221 DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN 276
                ++++ S+ N ++ + T Y + Y+++F L YN+ Y +FN
Sbjct: 974 N----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFN 1024
                                                               1197 AA
tr
     Q9ZAJ9
                       Ntnh protein [ntnh] [Clostridium
     Q9ZAJ9_CLOBO
                    botulinum]
                                                                <u>align</u>
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)
Query: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
          + T++T LI K E +DNN + D+SG V+ D + L
Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
                     V+ + N + FS+ FW+R
                                             NG ++ I ++ +I
Sbjct: 875 DALYLKEPDESVSFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926
Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
                  N +++++ID NG ++++ +S+ I++ W++++I+ + N I
Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978
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Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
          +IN KL +N I+ I + ++ I ++ I*+ SI N ++ * Y
Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVVNNYF 1033
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
              + Y++D G L YNK Y ++N N N Y+ +K
Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNNIYLSIK 1081
tr <u>P71117</u> Nontoxic-nonhemagglutinin [nontoxic-nonhemagglutinin]
   P71117 CLOBO [Clostridium
                                                                  AA
              botulinum]
                                                                  align
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)
+ T++T LI K E
                                   +DNN + D+SG V+ D + L
Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
                    V+ * N * FS+ FW+R N G ++ I ++ +I +N
Sbjct: 875 DALYLKEPDESVSFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926
Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
          GW+I N ++++++D NG ++++ + +S+ I++ W++++I+ + N I
Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978
Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
          +IN KL +N I+ I + ++ I ++ SIN ++ + Y
Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVVNNYF 1033
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
             + Y++D G L YNK Y ++N
                                            N N \lambda + +K
Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNNIYLSIK 1081
    087710
                      NTNH protein [ntnh] [Clostridium baratii] 1160 AA
    087710 9CLOT
Score = 74.3 bits (181), Expect = 5e-12
 Identities = 87/357 (24%), Positives = 157/357 (43%), Gaps = 50/357 (14%)
Query: 6 LKTIMPFDLSIYTNDTILIE----MFNKYN-----SEXXXXXXXXXXXXXYKDNNLI-DLS 53
          L+ IM L+ D + IE +FN Y
                                          S
                                                     + +D N+I D S
Sbjct: 759 LQLIMQNSLNSLNFDFLDIEKIKCLFNSYTRLLIKKQSSPYELSLYAFQGEDKNVIGDGS 818
Query: 54 GYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFWIRIP 109
          G VE + + L N + +N + T + +N + NS FS+FW+R
Sbjct: 819 GKNTLVEYTNDIGLIYGINNNALYLNQSNQSVSFTNDYFENGLTNS----FSIYFWLR-- 872
Query: 110 KYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI 169
              D I++ +I+ +N GW+I + N +++ +ID NG K ++ I
Sbjct: 873 NLGKDIIKS----- KLISSKLDNCGWEIYLEDNGLVFNIIDSNGSYKKIY-----I 918
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Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
          +IN KL +N I+ I + ++ I ++ SI N ++ + Y
Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVVNNYF 1033
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
             + Y++D G L YNK Y ++N N N Y+ +K
Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNNIYLSIK 1081
tr P71117 Nontoxic-nonhemagglutinin [nontoxic-nonhemagglutinin]
                                                               1197
   P71117 CLOBO [Clostridium
                                                                AA
              botulinum]
                                                                align
 Score = 74.3 bits (181), Expect = 5e-12
Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)
Ouery: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
          + T++T LI K E +DNN + D+SG V+ D + L
Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
                   V+ * N * FS+ FW+R N G ++ I ++ +I +N
Sbjct: 875 DALYLKEPDESVSFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926
Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
          GW+I N ++++++D NG ++++ + +S+ I++ W++++I+ + N I
Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978
Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
          +IN KL +N I+ I + ++ I ++ SIN ++ Y
Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVVNNYF 1033
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
             + Y++D G L YNK Y ++N N N Y+ +K
Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNNIYLSIK 1081
                     NTNH protein [ntnh] [Clostridium baratii] 1160 AA
    087710
tr
    087710 9CLOT
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 87/357 (24%), Positives = 157/357 (43%), Gaps = 50/357 (14%)
L+ IM L+ D + IE +FN Y S + +D N+I D S
Sbjct: 759 LQLIMQNSLNSLNFDFLDIEKIKCLFNSYTRLLIKKQSSPYELSLYAFQGEDKNVIGDGS 818
Query: 54 GYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFWIRIP 109
          G VE + + L N + +N + T + +N + NS FS+ FW+R
Sbjct: 819 GKNTLVEYTNDIGLIYGINNNALYLNQSNQSVSFTNDYFENGLTNS----FSIYFWLR-- 872
Query: 110 KYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI 169
              D I++ +I+ *N GW+I * N +++ *ID NG K ++
Sbjct: 873 NLGKDIIKS-----KLISSKLDNCGWEIYLEDNGLVFNIIDSNGSYKKIY------ 918
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Query: 170 SEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQF 227
          S+ N W ++ I+ * I++N L *N DIKDI + ++ I *
Sbjct: 919 SDMNNSWNYIAISVDRLKEQLLIFVNDVLVANEDIKDILNIYSSNTISL----VSENNQ 973
Query: 228 IWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN-AGNKNSYIKL 286
          I ++ SI NT +++ + Y + Y+++ L YNK+Y +FN +K K+
Sbjct: 974 ICIEGLSILNTNITKEEVLNNYFADLNNSYIRNGNEERLEYNKKYNLFNYVFSKTPICKV 1033
Query: 287 KKDSPVGEILTRSKYNQNSKYINYRDLYI--GEKFIIRRKSNSQSINDDIVRKEDYI 341
            ++ + + + N N K +++ L + +K++ + SI DD
Sbjct: 1034 NHNNKI-YLSINNDDNLNVKPLSFMLLSVDSNKKYVQKCDEVIISILDD---KERYL 1086
tr 069277 Nontoxic-nonhaemagglutinin [ntnh] [Clostridium
                                                                    1198
   O69277_CLOBO botulinum]
                                                                    AA
                                                                   <u>align</u>
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NO+I F** F + FS+ FW+R D I++ +I ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAK--IYINGKLESN 199
             +++ +ID NG K+++ D+S N W ++TI+ + + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            TK+I + ++ I ++ T+++ SIN ++ Y + Y++
Sbjct: 989 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVVNNYFTYLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
          D G P ANK A ++M N M A+ +K
Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTENNNIYLSIK 1082
tr 033871 • Nontoxic-nonhemagglutinin component [ntnh/B]
                                                                    1197
                                                                    AΑ
   O33871 CLOBO [Clostridium botulinum]
                                                                    <u>align</u>
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)
Query: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXXXYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
           + T++T LT K E +DNN + D+SG V+ D + L
Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
                     V++ N+ FS+ FW+R NG++ I++ +I
Sbjct: 875 DALYLKEPDESVSFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926
Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
           GW+I N +++**+D NG *+++ + +S* I++ W+***I+ + N
```

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Query: 170 SEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQF 227
           S+ NW++I+ * I*+N L*N DIKDI +++ I *
Sbjct: 919 SDMNNSWNYIAISVDRLKEQLLIFVNDVLVANEDIKDILNIYSSNTISL----VSENNQ 973
Query: 228 IWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN-AGNKNSYIKL 286
           I ++ SI NT +++ + Y + Y+++ L YNK+Y +FN +K K+
Sbjct: 974 ICIEGLSILNTNITKEEVLNNYFADLNNSYIRNGNEERLEYNKKYNLFNYVFSKTPICKV 1033
Query: 287 KKDSPVGEILTRSKYNONSKYINYRDLYI--GEKFIIRRKSNSOSINDDIVRKEDYI 341
            ++ + + . + N N K +++ L + +K++ + SI DD KE Y+
Sbjct: 1034 NHNNKI-YLSINNDDNLNVKPLSFMLLSVDSNKKYVQKCDEVIISILDD---KERYL 1086
tr 069277 Nontoxic-nonhaemagglutinin [ntnh] [Clostridium
   O69277 CLOBO botulinum]
                                                                   AA
                                                                   align
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)
Ouerv: 88
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+I F*+F+ FS+ FW+R D I++ +I ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAK--IYINGKLESN 199
             +++ +ID NG K+++ D+S NW ++TI+ + + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           IK+I + ++ I ++ II+++ SIN ++ + Y + Y++
Sbjct: 989 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVVNNYFTYLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
          D = G = F \times XNK \times X + + K
N = N \times X + + K
Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTENNNIYLSIK 1082
tr 033871 Nontoxic-nonhemagglutinin component [ntnh/B]
                                                                   1197
   O33871_CLOBO [Clostridium botulinum]
                                                                   AΑ
                                                                   align
 Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)
Query: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLI--DLSGYGAKVEVYDGVELNDKNOF 73
          + T++T LT K E
                                     +DNN + D+SG V+ D + L
Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
                    V+ + N + FS+ FW+R N G ++ I ++ +I
Sbjct: 875 DALYLKEPDESVSFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926
Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
```

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Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978
Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
          +IN KL +N I+ I + ++ I ++ I+++ SI N ++
Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVVNNYF 1033
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
              + Y++D G L YNK Y ++N N N Y+ +K
Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNNIYLSIK 1081
    Q45893
    Q45893 NTNH protein [ntnh] [Clostridium Q45893_CLOBO botulinum]
                                                             1198 AA
tr
                                                               align
Score = 73.9 \text{ bits} (180), Expect = 7e-12
Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAK--IYINGKLESN 199
            - +++ +ID NG K+++ D+S N W ++TI+ + + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            IK+T + ++ T ++ IL++ SI M ++ + Y + Y++
Sbjct: 989 GSIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVVNNYFTYLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
          D G L YNK Y ++N
Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTENNNIYLSIK 1082
                        NTNHA [ntnha] [Clostridium botulinum] 1196 AA
tr
    Q9LBR2
     Q9LBR2 CLOBO
                                                           align
 Score = 73.6 bits (179), Expect = 9e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)
Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
          R ++N+I D+SG ++ + VEL
                                   Sbjct: 843 RGPNSNIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900
Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
                    K+D I N+ NN GW+I N +++ +ID NG +SV
Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952
Query: 160 FFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
              I NW+++I++ + I+INK +N I+I + + I
Sbjct: 953 YLSNVIN-----NNWYYISISVDRLKDQLLIFINDKNVANVSIEQILNIYSTNVISL- 1004
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
             ++* I++* S+ + ** + * Y + Y++D * L YNK Y ++N
Sbjct: 1005 ----VNKNNSIYVEELSVLDKPVASEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNY 1060
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Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978
Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
          +IN KL +N I+ I + ++ I ++
                                           I+++ SI N ++
Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVVNNYF 1033
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
              + Y++D G L YNK Y ++N
                                             N N Y+ +K
Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNNIYLSIK 1081
                                                               1198 AA
                       NTNH protein [ntnh] [Clostridium
    Q45893
    Q45893_CLOBO
                       botulinum]
                                                                align
Score = 73.9 bits (180), Expect = 7e-12
Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
Query: 88
          NQ+I F++ F + FS+ FW+R
                                      D I++ +I ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAK--IYINGKLESN 199
             +++ +ID NG K+++ D+S N W ++TI+ + + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            IK+I + ++ I ++ I+++ SI N ++ + Y + Y++
Sbjct: 989 GSIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVVNNYFTYLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
          D G L YNK Y ++N
                                      N N Y+ +K
Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTENNNIYLSIK 1082
                         NTNHA [ntnha] [Clostridium botulinum] 1196 AA
     Q9LBR2
t.r
                                                             align
     Q9LBR2 CLOBO
 Score = 73.6 bits (179), Expect = 9e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)
Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
          R ++N+I D+SG ++ + VEL +
                                            S N + + N N + +
Sbjct: 843 RGPNSNIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900
Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
          F++ FW+R K+D I N+ NN GW+I N ·+++ +ID NG +SV
Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952
Query: 160 FFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
              I NW+*++I+ + + I+INK +N I+I * + I
sbjct: 953 YLSNVIN-----NNWYYISISVDRLKDQLLIFINDKNVANVSIEQILNIYSTNVISL- 1004
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
              ++* I+++ S+ + *+ + Y + Y++D * L YNK Y ++N
Sbjct: 1005 ----VNKNNSIYVEELSVLDKPVASEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNY 1060
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Query: 277 -----AGNKNSYIKLK 287
                     N SY+ LK
Sbjct: 1061 VFPETSLYEVNDNNKSYLSLK 1081
sp P46081
                                                                   1196
             Botulinum neurotoxin type C1, nontoxic component
   BXCN CLOBO [Clostridium
                                                                   AΑ
             botulinum]
                                                                   align
 Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)
          NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
Query: 47
          N \div D \div SG + + + \div EL + SN T + + N \div + F + F
Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905
Query: 105 WIRIPKYKNDGIONYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164
                KND I N+ NN GW+I N +++ +ID NG +SV+
Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956
Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
          Sbjct: 957 IIND------NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL-----V 1005
Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
           ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065
Query: 277 ----AGNKNSYIKLK 287
                 N SY+ LK
Sbjct: 1066 SLYEVNDNNKSYLSLK 1081
     Q93HT4
tr
                        NTNHA [ntnha] [Clostridium botulinum] 1196 AA
     Q93HT4 CLOBO
                                                            align
Score = 72.0 bits (175), Expect = 3e-11
Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)
Query: 47
          NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
          N + D+SG ++ + +EL
                               + S N I+ + N + +F++ F
Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905
Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164
                KND I N+ NN GW+I N +++ +ID NG +SV+ N
Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956
Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
          I D W++++I+ + + I+IN K +N I I + + I
```

Sbjct: 957 IIND-----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276

++ I \* ++ S+ \* ++ \* Y + Y++D + L YNK Y ++N
Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1061 VFPETSLYEVNDNNKSYLSLK 1081

N SY+ LE

Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

sp <u>P46081</u> 1196 Botulinum neurotoxin type C1, nontoxic component BXCN CLOBO [Clostridium AΑ botulinum] align Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 Query: 47  $N \div D \div SG + + + + \pm EL + S N T + + N \div + \pm E + E$ Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N+ NN GW+I N +++ +ID NG +SV+ N Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL-----V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I+++ S+ + ++ + Y + Y++D + L YMK Y ++MSbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065 Query: 277 ----AGNKNSYIKLK 287

tr  $\frac{Q93HT4}{Q93HT4}$  CLOBO

NTNHA [ntnha] [Clostridium botulinum] 1196 AA align

Score = 72.0 bits (175), Expect = 3e-11

Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
N + D+SG ++ + + &L + S N I+ + N + + &+ & E

Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164
W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N

Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W+++++I+ + + I+IN K +N I I + + I + + Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
++ I\*++ S+ \* ++ \* Y + Y++D + L YNK Y ++N
Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 ----AGNKNSYIKLK 287
N SY+ LK

Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q45916 138kDa protein associated with BoNT /C1-haemagglutinin 1196 Q45916 CLOBO complex align [CHn-138] [Clostridium botulinum] Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 N + D + SG + + + + EL +S N T+ + N + +F++ F Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N+ MN GW+I N +++ +ID NG +SV+ Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W++++I+ + + I+INK +N I I + + I + Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I+++ S+ + ++ + Y + Y++D + L YMK Y ++MSbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 ----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q9ZX77 NTNH [ntnh] [Clostridium botulinum D 1196 AA Q9ZX77\_CBDP bacteriophage] align

Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 N + D+SG ++ + +EL + S N I+ + N + +F++ F

Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164

W+R KND T N+ NN GW+T N +++ +1D NG +SV+ N
Sbjct: 906 WLRFTG-KNDDKTRLIGNKV------NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222

Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I\*++ S+ \* ++ \* Y + Y++D + L YNK Y ++N

Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 ----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr <u>Q45916</u> 138kDa protein associated with BoNT /C1-haemagglutinin 1196 Q45916 CLOBO complex [CHn-138] [Clostridium botulinum] align Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 N + D+SG ++ + +EL + S N T+ + N + +F++ F Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N+ NN GW+I N +++ +ID NG +SV+ Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W++++I+ + + I+IN K +N I I + + I + Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I+++ S+ + ++ + Y + Y++D + 5 YNK Y ++M Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065 Query: 277 ----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

Q9ZX77 1196 AA NTNH [ntnh] [Clostridium botulinum D Q9ZX77\_CBDP bacteriophage] <u>align</u> Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 Query: 47 N + D + SG ++ + + EFL + SN I+ + N + +F++ FSbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 WHR KND I N+ NN GW+I N +++ +ID NG +SV+ Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W++++I+ + + I+INK +N I I + + I Sbjct: 957 IIND------V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 ----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q38197 ANTP-139 protein [ANTP-139] [Clostridium botulinum 1196 Q38197\_9VIRU **phage 1C**] AA · align Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 N + D+SG ++ + +EL + SN T+ + N + +F++ F Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N+ NN GW+I N +++ +ID NG +SV+ N Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W+++I+ + + I+IN K +N I I + + I Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065 Query: 277 -----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q53550 Progenitor toxin L nontoxic-nonhemagglutinin component Q53550 CLOBO [Clostridium AΑ botulinum] align Score = 71.6 bits (174), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 N + D+SG ++ + +EL + S N I+ + N + +F++ F Sbjct: 848 NIIEDISGKNTFIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N+ NN GW+I N +++ +ID NG +SV+ N Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W++++I+ + + I+IN K +N I I + + I + Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276

++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N

Query: 277 ----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

1196 tr <u>Q38197</u> ANTP-139 protein [ANTP-139] [Clostridium botulinum Q38197 9VIRU phage 1C] AA align Score = 72.0 bits (175), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 Query: 47 N + D+SG ++ + +EL + S N T+ + N + +F++ F Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Ouery: 105 WIRIPKYKNDGIONYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N÷ NN GW+I N +++ +ID NG +SV+ N Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W++++I+ + + I+INK +N I I + + I + Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005 Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I+++ S+ + ++ + Y + Y++D + L YMK Y ++N Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065 Query: 277 ----AGNKNSYIKLK 287 N SY+ LK Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

Q53550 CLOBO [Clostridium AA align botulinum] Score = 71.6 bits (174), Expect = 3e-11Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%) Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104 N + D+SG ++ + +EL + S N I+ + N + +F++ F Sbjct: 848 NIIEDISGKNTFIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905 Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN 164 KND I N+ NN GW+I N +++ +ID NG +SV+ N Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956 Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222 I D W++++I\* + + I+IN K +N I I + + I + Sbjct: 957 IIND-----NWYYISISVDRLKDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276 ++ I\*++ S+ \* ++ \* Y + Y++D + L YNK Y ++N

Progenitor toxin L nontoxic-nonhemagglutinin component

tr Q53550

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Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065
Query: 277 ----AGNKNSYIKLK 287
                N SY+ LK
Sbjct: 1066 SLYEVNDNNKSYLSLK 1081
                                                             1161 AA
    Q45891
tr
                      NTNH protein [ntnh] [Clostridium
    Q45891 CLOBO
                                                              align
Score = 70.9 bits (172), Expect = 6e-11
 Identities = 70/291 (24%), Positives = 127/291 (43%), Gaps = 49/291 (16%)
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
Query: 88
          NQ+I F++ F+ F+ FS+ FW+R D I++ +I ++N GW+T+
Sbjct: 852 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 903
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S N W ++TI+ +
Sbjct: 904 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTELSOSNIEERYKIOSYSEYLK 259
            Sbjct: 957 ESIKEILNIYSSNTISL----VDENNPIYVEGLSILNKPTTSQEVLSNYFKVLNNSYIR 1011
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSK---YNONS 305
          D L YNK Y ++N N N Y++ ++ +++ K N N
Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNLQVSKFKLLSINPNK 1071
Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
          +Y+ D I EK+I I + Q I++ K+ I D F N
Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1122
    Q45880
                      NtnhA protein [ntnhA] [Clostridium 1193 AA
    Q45880 NtnhA proto botulinum]
                                                              <u>align</u>
Score = 68.9 bits (167), Expect = 2e-10
Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%)
Query: 88
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+T F++ F + FS+ FW+R D T++ +1 ++N GW+T +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S NW ++TI+ + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           IK+I + ** I ++ I+++ SIN + + Y + Y**
Sbjct: 989 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNKPTTSQEVLSNYFKVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSK---YNQNS 305
               L YNK Y **N N N Y+ + + + + + + K N N
```

Sbjct: 1044 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNLQVSKFKLLSINPNK 1103

```
Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065
Query: 277 ----AGNKNSYIKLK 287
                 N SY+ LK
Sbjct: 1066 SLYEVNDNNKSYLSLK 1081
tr
     Q45891
                                                                 1161 AA
                        NTNH protein [ntnh] [Clostridium
     Q45891 CLOBO
                                                                  align
 Score = 70.9 bits (172), Expect = 6e-11
 Identities = 70/291 (24%), Positives = 127/291 (43%), Gaps = 49/291 (16%)
           NQNIIFNSVFLD----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
Query: 88
           \texttt{NQ+I} \ \ \texttt{F++} \ \ \texttt{F} \ \ + \\ \texttt{ES+} \ \ \texttt{FW+R} \qquad \qquad \texttt{D} \ \ \texttt{I++} \\ + \texttt{I} \quad \  + \texttt{H} \ \ \texttt{GW+I} \quad + \\
Sbjct: 852 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 903
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
             +++ +ID NG K+++ D+S N W ++TI+ +
Sbjct: 904 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            Sbjct: 957 ESIKEILNIYSSNTISL----VDENNPIYVEGLSILNKPTTSQEVLSNYFKVLNNSYIR 1011
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSK---YNONS 305
           D LYNKY ++N NNY++ ++ +++ K NN
Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNLQVSKFKLLSINPNK 1071
Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
           +Y+ D I EK+I I + Q I++ K+ I D F N
Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1122
     Q45880
                       NtnhA protein [ntnhA] [Clostridium
                                                                 1193 AA
    Q45880 CLOBO botulinum]
                                                                  align
Score = 68.9 bits (167), Expect = 2e-10
Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%)
Query: 88
           NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
           NQ+T F++ F + FS+ FW+R D T++ +1 ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S NW ++TI+ + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           Sbjct: 989 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNKPTTSQEVLSNYFKVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSK---YNQNS 305
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L YNK Y \*\*N N N Y+ + + + +++ K N N

Sbjct: 1044 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNLQVSKFKLLSINPNK 1103

+Y+ D I EK+I I + Q I++ K+ I D F N Sbjct: 1104 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154 tr 069276 Nontoxic-nonhaemagglutinin [ntnh] [Clostridium 1161 069276 CLOBO botulinum] AΑ align Score = 68.9 bits (167), Expect = 2e-10Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%) Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141 Sbjct: 852 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 903 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199 +++ +ID NG K+++ D+S N W ++TI+ + I+T+ L +N Sbjct: 904 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956 Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259  $IK+I + ++ \cdot I \qquad \qquad ** \qquad I+** \quad SI \quad N \quad + \quad + \quad Y \qquad + \quad Y++$ Sbjct: 957 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNKPTTSQEVLSNYFKVLNNSYIR 1011 Query: 260 DFWGNPLMYNKEYYMFN------AGNKNSYIKLKKDSPVGEILTRSK---YNQNS 305 Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNLQVSKFKLLSINPNK 1071 Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349 +Y+ D I EK+I I + Q I++ K+ I D F N Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1122 tr <u>Q45887</u> Botulinum neurotoxin type F nontoxic-nonhemaglutinin 1165 Q45887 CLOBO component [ntnh] AΑ [Clostridium botulinum] <u>align</u> Score = 67.8 bits (164), Expect = 5e-10Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%) Query: 45 KDNNLI-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLD--- 99 +DNN+I D SG VE G+EL + NS + + NO+LIE + + + Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNGSNQSIIFTNDYFENGL 865 Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT 156 FS+ FW+R N G Q+ T ++ +T + N GW+I + ++ +ID NG Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917 Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214 K+++ D+S N W ++TI+ + I+I+ L N IKDI + ++ I Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVNESIKDILNIYSSNII 970 Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYM 274 \*\*+ +I N + \* Y + Y++D L YNK Y +

Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349

Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349 +Y+ D I EK+I I + Q I++ K+ I D F N Sbjct: 1104 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154 tr <u>069276</u> 1161 Nontoxic-nonhaemagglutinin [ntnh] [Clostridium 069276 CLOBO botulinum] AΑ align Score = 68.9 bits (167), Expect = 2e-10Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%) NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141 Query: 88 NQ+1 F++ F + FS+ FW+R D I++ +1 ++N GW+T + Sbjct: 852 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 903 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199 +++ +ID NG K+++ D+S N W ++TI+ + Sbjct: 904 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956 Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTELSOSNIEERYKIOSYSEYLK 259 Sbjct: 957 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNKPTTSQEVLSNYFKVLNNSYIR 1011 Query: 260 DFWGNPLMYNKEYYMFN------AGNKNSYIKLKKDSPVGEILTRSK---YNQNS 305 D E YNK Y ++N N N Y++ + + +++ K N N Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNLQVSKFKLLSINPNK 1071 Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349 +Y+ D I EK+II + Q I++ K+ I D F N Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1122 tr Q45887 Botulinum neurotoxin type F nontoxic-nonhemaglutinin 1165

Q45887 CLOBO component [ntnh] AA[Clostridium botulinum] <u>align</u> Score = 67.8 bits (164), Expect = 5e-10Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%) Query: 45 KDNNLI-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLD--- 99 +DNN+I D SG VE G+EL + NS + + NO+LIE + + + Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNGSNQSIIFTNDYFENGL 865 Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT 156 FS+ FW+R N G Q+ T ++ +T + N GW+I + ++ +ID NG Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917 Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214 K+++ D+S N W ++TI+ + T+T+ L N IKDT + ++ T Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVNESIKDILNIYSSNII 970 Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYM 274 \*\*+ +I N + \* X + X++D I YNK Y +

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Sbjct: 971 SLLSDNKAS----YIEGLTILNKPTTGEEVLRNYFKNLNNSYVRDSNDERLEYNKTYQL 1025
Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR------SKYNQNSKYINYRD-----LY 314
                    ++K+D+ + +
                 N
                                                 N N +Y+
Sbjct: 1026 YDYVFPDNPICEVKQDNNIYLTINNINNLNMKPCKFKLLSINSNKQYVQKWDEVIISVLY 1085
Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
             EK++ I *+N I D+ + + *I
Sbjct: 1086 DTEKYVCISNENNRVKIIDNKIMQVKFI 1113
tr Q45844
               Neurotoxin complex M nontoxic-nonhemagglutinin
                                                                     1165
   Q45844 CLOBO component [NTNH]
                                                                    AΑ
                [Clostridium botulinum]
                                                                    align
 Score = 67.8 bits (164), Expect = 5e-10
 Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%)
Query: 45
           KDNNLI-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-ONONIIFNSVFLD--- 99
           +DNN+I D SG VE G+EL + NS + + NQ+IIE + + +
Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNGSNQSIIFTNDYFENGL 865
Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT 156
             FS+ FW+R N G Q+ I ++ +I + N GW+I + ++ +ID NG
Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917
Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214
           K+++ D+S N W ++TI+ + I+I+ L N IKDI + ++ I
Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVNESIKDILNIYSSNII 970
Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYM 274
                     Sbjct: 971 SLLSDNKAS----YIEGLTILNKPTTGEEVLRNYFKNLNNSYVRDSNDERLEYNKTYQL 1025
Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR------SKYNONSKYINYRD-----LY 314
                 N ++K+D+ + +
                                                N N +Y+ D
Sbjct: 1026 YDYVFPDNPICEVKQDNNIYLTINNINNLNMKPCKFKLLSINSNKQYVQKWDEVIISVLY 1085
Query: 315 IGEKFI-IRRKSNSOSINDDIVRKEDYI 341
             EK++ I ++N I D+ + + +I
Sbjct: 1086 DTEKYVCISNENNRVKIIDNKIMQVKFI 1113
tr
    Q564H3
                        Neurotoxin heavy chain [Clostridium sp.
                                                                  167 AA
    Q564H3 9CLOT
                        RKD]
                                                                  align
 Score = 63.5 bits (153), Expect = 9e-09
 Identities = 50/167 (29%), Positives = 71/167 (41%), Gaps = 13/167 (7%)
Query: 301 YNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXX 360
                I YR LY G KFII+R + + I D V+ D+I L N E V
Sbjct: 9 YTNGKLNIYYRRLYNGLKFIIKRYTPNNEI-DSFVKSGDFIKLYVSYNNNEHIVGYPKDG 67
Query: 361 XXXXXXXXAPI---SDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRF 417
                      * Y ++ + * TYS QL D+ *+ +GL+G H
```

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Sbjct: 971 SLLSDNKAS----YIEGLTILNKPTTGEEVLRNYFKNLNNSYVRDSNDERLEYNKTYQL 1025
Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR------SKYNQNSKYINYRD-----LY 314
                N
                   ++K+D+ + +
                                                 別 以 4天十
                                                         D
Sbjct: 1026 YDYVFPDNPICEVKQDNNIYLTINNINNLNMKPCKFKLLSINSNKQYVQKWDEVIISVLY 1085
Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
            EK++ I **N I D* + + *I
Sbjct: 1086 DTEKYVCISNENNRVKIIDNKIMQVKFI 1113
               Neurotoxin complex M nontoxic-nonhemagglutinin
                                                                    1165
tr Q45844
   Q45844 CLOBO component [NTNH]
                                                                    AA
               [Clostridium botulinum]
                                                                    align
Score = 67.8 bits (164), Expect = 5e-10
Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%)
          KDNNLI-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLD--- 99
Query: 45
           +DNN+I D SG VE G+EL + NS + + NQ+IIF + + +
Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNGSNQSIIFTNDYFENGL 865
Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT 156
            FS+ FW+R NGQ+ I ++ +I + NGW+I + ++ +ID NG
Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917
Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214
                  D+S NW++TI++ I+I+ L N IKDI + ++ I
Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVNESIKDILNIYSSNII 970
Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYM 274
                    +++ +I N + + Y + Y++D
Sbjct: 971 SLLSDNKAS----YIEGLTILNKPTTGEEVLRNYFKNLNNSYVRDSNDERLEYNKTYQL 1025
Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR-----SKYNQNSKYINYRD-----LY 314
                N ++K+D+ + +
                                                N N +Y+ D
Sbjct: 1026 YDYVFPDNPICEVKQDNNIYLTINNINNLNMKPCKFKLLSINSNKQYVQKWDEVIISVLY 1085
Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
            EK++ I ++N I D+ + + +I
Sbjct: 1086 DTEKYVCISNENNRVKIIDNKIMQVKFI 1113
    Q564H3
                       Neurotoxin heavy chain [Clostridium sp.
tr
                                                                  167 AA
    Q564H3_9CLOT
                                                                  align
                       RKD]
Score = 63.5 bits (153), Expect = 9e-09
Identities = 50/167 (29%), Positives = 71/167 (41%), Gaps = 13/167 (7%)
Query: 301 YNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTXXXX 360
                I YR LY G KFII+R + + I D V+ D+I L N E V
Sbjct: 9 YTNGKLNIYYRRLYNGLKFIIKRYTPNNEI-DSFVKSGDFIKLYVSYNNNEHIVGYPKDG 67
Query: 361 XXXXXXXXAPI~~-SDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRF 417
                    + + Y ++ + + TYS QL D+ ++ +GL+G H
```

```
Query: 418 YESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWT 464
             I + +D S WY +K K LGC+W F+F DEGWT
Sbjct: 125 --GQIGNDPNRDILIASNWYFNHLKDKI----LGCDWYFVPTDEGWT 165
     Q9ZAJ6
                                                               1162 AA
     Q9ZAJ6_CLOBO Ntnh prote botulinum]
tr
                       Ntnh protein [ntnh] [Clostridium
                                                                 align
 Score = 63.5 bits (153), Expect = 9e-09
 Identities = 70/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
           NQ+1 F++ F + FS+ FW+R N G + +1 ++N GW+I +
Sbjct: 849 NQSISFSNDFFENGLTNSFSIHFWLR----NLGQDT---TKSKLIGSKEDNCGWEIYFQ 900
'Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S N W ++TI+ + I+I+ L N
Sbjct: 901 NTGLVFNMIDSNGDEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVN 953
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            IK+I + ++ I D + +*+ +I N + + Y + Y++
Sbjct: 954 ESIKEILNIYSSNIISLLSDNNAS----YIEGLTILNKPTTGEEVLSNYFKNLNNSYIR 1008
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
           D L YNK Y ++N N N Y++ ++ L SK+ N
Sbjct: 1009 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1066
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
           N + Y + D I   EK + I I + Q_A I + + K + I D F N
Sbjct: 1067 NKQYVQKFDEVIISVLDNMEKYIDISEDNRLQLIDNKNSAKKMIISNDIFISN 1119
                Type A progenitor toxin nontoxic-nonHA (NTNH) [ant] 1193
tr Q45914
   Q45914 CLOBO [Clostridium
                                                                    AΑ
                botulinum]
                                                                    align
 Score = 63.2 \text{ bits } (152), \text{ Expect} = 1e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
           NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S N W ++TI+ + I+I+ I: +N -
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            IK+I + ** I + +++ *IN * + Y + Y**
Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLSNYFEVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
           D L YNK Y ++N
                                      NNY++++ LSK+
```

Sbjct: 68 NAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNAS--LGLVGTHN- 124

```
Query: 418 YESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWT 464
             I + +D S WY +K K LGC+W F+P DEGWT
Sbjct: 125 --GQIGNDPNRDILIASNWYFNHLKDKI----LGCDWYFVPTDEGWT 165
tr
     Q9ZAJ6
                       Ntnh protein [ntnh] [Clostridium
                                                              1162 AA
     Q9ZAJ6 CLOBO
                       botulinum]
                                                               aliqn
 Score = 63.5 bits (153), Expect = 9e-09
 Identities = 70/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+I F++ F + FS+ FW+R N G + +I ++N GW+I +
Sbjct: 849 NQSISFSNDFFENGLTNSFSIHFWLR----NLGQDT---TKSKLIGSKEDNCGWEIYFQ 900
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
             +++ +ID NG K+++ D+S N W ++TI+ + T+T+ L N
Sbjct: 901 NTGLVFNMIDSNGDEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVN 953
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            Sbjct: 954 ESIKEILNIYSSNIISLLSDNNAS----YIEGLTILNKPTTGEEVLSNYFKNLNNSYIR 1008
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
          D LYNKY ++N NNY++ ++ LSK+ N
Sbjct: 1009 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1066
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
          N + Y + D = I EK + I = I + Q + I + E + I = D + N
Sbjct: 1067 NKQYVQKFDEVIISVLDNMEKYIDISEDNRLQLIDNKNSAKKMIISNDIFISN 1119
tr Q45914
               Type A progenitor toxin nontoxic-nonHA (NTNH) [ant]
                                                                  1193
   Q45914_CLOBO [Clostridium
                                                                  AA
               botulinum]
                                                                  a<u>lign</u>
 Score = 63.2 bits (152), Expect = 1e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
Query: 88
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+T F++ F + FS+ FW+R D T++ +I ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
             +++ +TD NG K+++ D+S N W ++TI+ + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           \exists K+I + ++ + I + +++ + \exists N + + + Y + + Y++
Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLSNYFEVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
              L YNK Y ++N
                                     NNY++++ LSK+
```

Sbjct: 68 NAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNAS--LGLVGTHN- 124

```
Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1101
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
           N +Y+ D I EK+I I + Q I++
Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154
tr
     P71107
                       Ntnh protein [ntnh] [Clostridium botulinum 1193 AA
     P71107 CLOBO
 Score = 63.2 bits (152), Expect = 1e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
Query: 88
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+I F++ F + FS+ EW+R D I++ +I ++N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
             +++ +ID NG K+++ D+S N W ++TI+ +
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSOSNIEERYKIOSYSEYLK 259
            Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLSNYFEVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
               L YNK Y ++N N N Y++ ++ L SK+ N
Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1101
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
          N +Y+ D I EK+II + Q I++ K+ I D F N
Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154
    Q45850 Ntnh protein [ntnh] [Clostridium Q45850_CLOBO botulinum]
                                                               1163 AA
                                                                <u>align</u>
 Score = 62.8 bits (151), Expect = 2e-08
 Identities = 49/214 (22%), Positives = 100/214 (45%), Gaps = 29/214 (13%)
Query: 88
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+T F++ F + FS+ FW+R D T++ +I
                                                      ++N 6M+I +
Sbjct: 850 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 901
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S N W ++TI+ + I+I+ L N
Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISIDRLKEQLLIFIDDNLVVN 954
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           IK+I + *+ I + +++ *I N + + X + X*+
Sbjct: 955 ESIKEILNIYSSNIISL----LSNNNASYIEGLTILNKPTTSQEVLSNYFKNLNNSYIR 1009
Query: 260 DFWGNPLMYNKEYYMFN-AGNKNSYIKLKKDSPV 292
                I. YNK Y **N ++N ++K+** +
Sbjct: 1010 DSNEERLEYNKTYQLYNYVFSENPIYEIKQNNNI 1043
```

```
Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1101
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
                D I
                          EK+II + QI++ K+ I DF N
          N +Y+
Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154
    P71107
                      Ntnh protein [ntnh] [Clostridium botulinum 1193 AA
tr
    P71107_CLOBO
                                                               align
Score = 63.2 bits (152), Expect = 1e-08
Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
Query: 88
          NQ+I F++ F+ + SS+ FW+R D I++ + +I ++R GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S N W ++TI+ +
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLSNYFEVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
          D L YNK Y ++N ' N N Y+ + + + L SK+ N
Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1101
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
          N +Y+ D I EK+I I + Q I++ E+ I D F N
Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154
                                                             1163 AA
    Q45850 Ntnh prote Q45850_CLOBÓ botulinum]
t.r
    Q45850
                      Ntnh protein [ntnh] [Clostridium
                                                               align
Score = 62.8 bits (151), Expect = 2e-08
Identities = 49/214 (22%), Positives = 100/214 (45%), Gaps = 29/214 (13%)
Query: 88
          NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+T F++ F + FS+ FW+R D T++ +I ++N GW+I +
Sbjct: 850 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 901
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S NW ++TI+ + I+I+ L N
Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISIDRLKEQLLIFIDDNLVVN 954
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            IK+I + ** I + +++ *I N + + Y + Y**
Sbjct: 955 ESIKEILNIYSSNIISL----LSNNNASYIEGLTILNKPTTSQEVLSNYFKNLNNSYIR 1009
Query: 260 DFWGNPLMYNKEYYMFN-AGNKNSYIKLKKDSPV 292
               L YNK Y **N ++N ++K+*+ +
Sbjct: 1010 DSNEERLEYNKTYQLYNYVFSENPIYEIKQNNNI 1043
```

1193

```
P71108 CLOBO botulinum]
                                                                AA
                                                                <u>align</u>
Score = 61.6 bits (148), Expect = 3e-08
Identities = 69/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
          NQ+I F++ F + FS+ FW+R D I++ +I +N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKGDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +TD NG K+++ D+S N W ++TT+ + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Ouery: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
           Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
          D LYNKY **N NNY++++ LSK+ N
Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINP 1101
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
          N +Y+ D I EE+I I + Q I++ K+ I D F N
Sbjct: 1102 NKQYVQKLDEVIISVLGNMEKYIDISEDNRLQLIDNKNGAKKMIISNDMFISN 1154
tr P71109
             Nontoxic-nonhemagglutinin [ntnh] [Clostridium
                                                                1159
   P71109 CLOBO botulinum]
                                                                AA
                                                                align
Score = 61.2 bits (147), Expect = 5e-08
Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
         NO*I F++ F * FS+ FW+R D I* Y +I +*N GW+I +
Sbjct: 850 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIK-----YKLIGSKEDNCGWEIYFQ 901
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
            +++ +ID NG K+++ D+S N W ++TI+ + I+I+ L +N
Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 954
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
            IK+1 + ++ I + +++++ +I N + + Y + +++
Sbjct: 955 ESIKEILNIYSSNIISL----LSENKPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1009
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
          Sbjct: 1010 DSNEERLEYHKTYQLDNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINS 1067
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
          N +Y+ D I
                         EK+II + QI++ K+ I DF N
```

tr P71108 Nontoxic-nonhemagglutinin component [Clostridium

```
tr P71108
                                                                                                                            1193
                            Nontoxic-nonhemagglutinin component [Clostridium
      P71108 CLOBO botulinum]
                                                                                                                            AA
                                                                                                                             align
 Score = 61.6 bits (148), Expect = 3e-08
 Identities = 69/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)
Query: 88
                    NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
                    NG+I F++ F + ES+ FW+R D I++ +I +N GW+I +
Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKGDNCGWEIYFQ 935
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
                        +++ +ID NG K+++ D+S NW ++TI+ + I+I+ L +N
Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
                     Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1043
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
                    D LYNKY **N NNY++++ LSK+
Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINP 1101
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
                    N +Y+ D I ÉK+II + Q I++ K+ I D F N
Sbjct: 1102 NKQYVQKLDEVIISVLGNMEKYIDISEDNRLQLIDNKNGAKKMIISNDMFISN 1154
tr <u>P71109</u>
                                                                                                                            1159
                           Nontoxic-nonhemagglutinin [ntnh] [Clostridium
     P71109_CLOBO botulinum]
                                                                                                                            AA
                                                                                                                            align
 Score = 61.2 bits (147), Expect = 5e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
Query: 88
                   NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
                    NQ+I F++ F + FS+ FW+R D I+ Y +I ++N GW+I +
Sbjct: 850 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIK-----YKLIGSKEDNCGWEIYFQ 901
Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
                        that the transfer of the trans
Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEOLLIFIDDNLVAN 954
Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLK 259
                       Sbjct: 955 ESIKEILNIYSSNIISL----LSENKPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1009
Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
                    D F A+K A + M
                                                                      N N Y+ + + + L SK+ N
Sbjct: 1010 DSNEERLEYHKTYQLDNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINS 1067
Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
                    N +Y+ D I
                                                 EK+II + QI++ K+ I DF N
```

## Sbjct: 1068 NKQYVQKFDEVIISILGNMEKYIDISEDNRLQLIDNKNGAKKMIISNDMFISN 1120

tr Q7WUH7 Botulinum neurotoxin type E (Fragment) [bont/E] 71 AA Q7WUH7\_CLOBU [Clostridium butyricum] align Score = 49.3 bits (116), Expect = 2e-04Identities = 30/77 (38%), Positives = 44/77 (56%), Gaps = 7/77 (9%) Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325 L+Y+KEYY+ N N++I + DS T S N S + LY G K I+R + Sbjct: 2 LLYDKEYYLLNVLKPNNFINRRTDS-----TLSINNIRSTILLANRLYSGIKVKIQRVN 55 Query: 326 NSQSINDDIVRKEDYIY 342 NS S ND++VR +D++Y Sbjct: 56 NS-STNDNLVRNDDHVY 71 tr Q8ILA2 Hypothetical protein [PF14 0343] [Plasmodium falciparum 2269 Q8ILA2 PLAF7 (isolate <u>align</u> 3D7)] Score = 48.1 bits (113), Expect = 4e-04Identities = 89/379 (23%), Positives = 144/379 (37%), Gaps = 73/379 (19%)

Query: 25 EMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGVELNDKN----- 71 E FNE ++E +Y +N LI+ Y K VY VE N+KN Sbjct: 1373 EDFNKLDNEHSKD-----KYGENALINYV-YLNKGNVYKNVEKNEKNKKNKERTHVNTEI 1426 Query: 72 ----QFKLTSSANSKIRVTQNQ----NIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122 Q K +S +NSK + N ++ F L + + +++ I Sbjct: 1427 KLNIYQRKESSDSNSKENIDMNNLECTSLYFTKNDLQNKNKLFDLLRNIDKKNLRDVIFK 1486 Query: 123 EYTIINCMKNNS---GWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179 + +IN + N G K + N I + K K+VF + + + Y NR Sbjct: 1487 IFAVINSKRFNGDMIGEKGKFKNNEITKYI----KNKNVFNKIKPYKKNTNYKNRK--- 1538 Query: 180 TITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF----- 233 Sbjct: 1539 --ENKKENKK---ENKKENKNNKKKLHSFFIRNKLIYNNNNNSNNNNICKNKNNIQKISK 1593 Query: 234 -SIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLM---YNKEYYMFNAGNK-----N 281 N +NI \*P Q E K+ GN + YN +Y + N NK Sbjct: 1594 QKKINKIFYPTNIYKRM-YQKIKENNKNMEGNQKIIETYNTKYKLINVPNKEIYFHKNEN 1652 Query: 282 SYIKLKKDSPVGEILTRSKYNQNSKYI----NYRDLYIGEKFIIRRKSNSQSINDDIVR 336 + I +KK PV + R Q +KYI NY L+I +K ++ NS + N+ I+ Sbjct: 1653 NNIGVKKTLPV--YIYRMTMKQKNKYIPIKKFNYSYLFIEKK---KKNYNSSTRNNKILP 1707

Query: 337 KEDYIYLDFFNLNQEWRVY 355
+ i.+ i. h + + y

Sbjct: 1708 YYYFFDLNNFTQNMKQNLY 1726

Sbjct: 1068 NKQYVQKFDEVIISILGNMEKYIDISEDNRLQLIDNKNGAKKMIISNDMFISN 1120

tr Q7WUH7 Botulinum neurotoxin type E (Fragment) [bont/E] 71 AA Q7WUH7\_CLOBU [Clostridium butyricum] align

Score = 49.3 bits (116), Expect = 2e-04Identities = 30/77 (38%), Positives = 44/77 (56%), Gaps = 7/77 (9%)

Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325 L+Y+KEYY+ N N++I + DS T S N S + LY G K I+R + Sbjct: 2 LLYDKEYYLLNVLKPNNFINRRTDS-----TLSINNIRSTILLANRLYSGIKVKIQRVN 55

Query: 326 NSQSINDDIVRKEDYIY 342 NS S ND++VR +D++Y Sbjct: 56 NS-STNDNLVRNDDHVY 71

tr Q8ILA2 Hypothetical protein [PF14\_0343] [Plasmodium falciparum 2269 Q8ILA2\_PLAF7 (isolate AA 3D7)]

Score = 48.1 bits (113), Expect = 4e-04Identities = 89/379 (23%), Positives = 144/379 (37%), Gaps = 73/379 (19%)

Sbjct: 1373 EDFNKLDNEHSKD----KYGENALINYV-YLNKGNVYKNVEKNEKNKKNKERTHVNTEI 1426

Query: 72 ----QFKLTSSANSKIRVTQNQ----NIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122 Q K +8 +NSK + N ++ F  $\Sigma$  + + +++  $\Sigma$ 

Sbjct: 1427 KLNIYQRKESSDSNSKENIDMNNLECTSLYFTKNDLQNKNKLFDLLRNIDKKNLRDVIFK 1486

Sbjct: 1487 IFAVINSKRFNGDMIGEKGKFKNNEITKYI----KNKNVFNKIKPYKKNTNYKNRK--- 1538

Query: 180 TITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF----- 233

N N K K E\* + K + + \*I+ + + \* K

Sbjct: 1539 --ENKKENKK---ENKKENKNNKKKLHSFFIRNKLIYNNNNNSNNNNICKNKNNIQKISK 1593

Query: 234 -SIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLM---YNKEYYMFNAGNK-----N 281 N +NI +P Q E K+ GN + YN +Y + N NK N

Sbjct: 1594 QKKINKIFYPTNIYKRM-YQKIKENNKNMEGNQKIIETYNTKYKLINVPNKEIYFHKNEN 1652

Query: 282 SYIKLKKDSPVGEILTRSKYNQNSKYI----NYRDLYIGEKFIIRRKSNSQSINDDIVR 336 + I +KK PV + R Q +KYI NY L+I +K ++ NS + N+ I+

Sbjct: 1653 NNIGVKKTLPV--YIYRMTMKQKNKYIPIKKFNYSYLFIEKK---KKNYNSSTRNNKILP 1707

Query: 337 KEDYIYLDFFNLNQEWRVY 355 + i...+ i..

Sbjct: 1708 YYYFFDLNNFTQNMKQNLY 1726

```
Score = 35.8 \text{ bits } (81), \text{ Expect = } 2.0
 Identities = 49/211 (23%), Positives = 89/211 (41%), Gaps = 19/211 (9%)
Query: 152 INGKTKSVFFEYNIRE----DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKD-IR 206
           Sbjct: 815 ISDSEENIHYESNIKDVNNYSSEHYLSDYCYDKNSSNYNNSEGYINNNVEKENDQYDEKR 874
Query: 207 EVIANGEIIFK-LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKI-----QSYSEYL 258
          + NG K DRQ YSI + + S++ + I
Sbjct: 875 SIQYNGNSYDKSYSYYSDRAQKDIYGYKSICSEDNSKNMNYSKDSIAIIKSITSANSEEK 934
Query: 259 KDF-WGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSK-YNQNSKYINYRDLYIG 316
           K+ + ++YN + N N NS+ L EI ++K * ++ * +Y
Sbjct: 935 KEMKYNKNIIYNNDCNDCNDYNVNSFYDLYDQEQFDEISQKNKIITRIGSFVTNKSVYQY 994
Query: 317 EKFIIRRKSNSQSINDDIVRKEDYIYLDFFN 347
                 K + S + I K D + D N
Sbjct: 995 EKY----KKDQSSTSVVIPSKYDTHFNDIEN 1021
tr Q8IBF4
                                                                     2773
               Hypothetical protein MAL7P1.167 [MAL7P1.167]
   Q8IBF4 PLAF7 [Plasmodium falciparum
                                                                    AA
               (isolate 3D7)]
                                                                     <u>aliqn</u>
 Score = 47.8 bits (112), Expect = 5e-04
 Identities = 82/340 (24%), Positives = 129/340 (37%), Gaps = 35/340 (10%)
Query: 21 TILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT-SSA 79
          T L + KY + Y NN I+ + G +
                                                     N +N KL S+
Sbjct: 44 TNLFKFNGKYENRIIHDDSTTNSYTPNNAIEKNNNGN----CNRSNNNTQNYIKLLQSNV 99
Query: 80 NSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN----EYTIINCMKNNSG 135
              T +N I N ++ + KN N I+N
Sbjct: 100 NFNKIKTPQENTIINLNKINQLHN-----KNQICSNRINNLCNYDEQLCNILNNNEK 151
Query: 136 WKISIRGNRIIWTLIDINGKTKSVFFEYN--IREDISEYINRWFFVTITNNLNNAKIYIN 193
           K + GN I T N T ++++ N T + S+YIN+ ++I N +N + + N
Sbjct: 152 DKKKLHGNNNIITHNHQNNITSTLYNYDNSCIENNQSDYINK---LSIKNKVNTSNTFYN 208
Query: 194 ----GKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERY 249
                   IK ÷
                            N + DG+ F
                                                + S + + · NI
Sbjct: 209 IDQFGLLNKKKKIKSLE----NLKSYISNDGESFNNSFTIKPFNSYNKSTMKVKNILSNE 264
Query: 250 KIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS-KYI 308
               + K+F N + N E+Y GN N+
                                           + 10
Sbjct: 265 KTILCRKNCKNFILNKRI-NLEHYNSKKGNSNNNDMNESDVVKNYKQDYGNNNNNSNNYY 323
Query: 309 NYRDLYIGEKFIIRRKSNSQSINDD-IVRKEDYIYLDFFN 347
           A D AI + +M +DD ++K ++IA L+M
Sbjct: 324 YYSDNYINDDDNNNYYNNYYYDDDDGDIKKGEHIY--FYN 361
tr Q7WRP2
               Botulinum neurotoxin type E (Fragment) [bont/E]
                                                                      71 AA
   Q7WRP2 CLOBU [Clostridium
               butyricum]
                                                                      align
```

```
Score = 35.8 \text{ bits } (81), \text{ Expect} = 2.0
 Identities = 49/211 (23%), Positives = 89/211 (41%), Gaps = 19/211 (9%)
Query: 152 INGKTKSVFFEYNIRE----DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKD-IR 206
              Sbjct: 815 ISDSEENIHYESNIKDVNNYSSEHYLSDYCYDKNSSNYNNSEGYINNNVEKENDQYDEKR 874
Query: 207 EVIANGEIIFK-LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKI-----QSYSEYL 258
           + NG K DRQ YSI + + S++ + I
Sbjct: 875 SIQYNGNSYDKSYSYYSDRAQKDIYGYKSICSEDNSKNMNYSKDSIAIIKSITSANSEEK 934
Query: 259 KDF-WGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSK-YNQNSKYINYRDLYIG 316
          K+ + ++YN + N N NS+ L EI ++K * ++ ++Y
Sbjct: 935 KEMKYNKNIIYNNDCNDCNDYNVNSFYDLYDQEQFDEISQKNKIITRIGSFVTNKSVYQY 994
Query: 317 EKFIIRRKSNSQSINDDIVRKEDYIYLDFFN 347
                K + S + I K D + D N
Sbjct: 995 EKY----KKDQSSTSVVIPSKYDTHFNDIEN 1021
tr <u>Q8IBF4</u>
               Hypothetical protein MAL7P1.167 [MAL7P1.167]
                                                                    2773
   Q8IBF4 PLAF7 [Plasmodium falciparum
                                                                    AΑ
               (isolate 3D7)]
                                                                    align
 Score = 47.8 bits (112), Expect = 5e-04
Identities = 82/340 (24%), Positives = 129/340 (37%), Gaps = 35/340 (10%)
Query: 21 TILIEMFNKYNSEXXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT-SSA 79
          TL+ KY+ Y NN I++ G +
                                                     N +N KL S+
Sbjct: 44 TNLFKFNGKYENRIIHDDSTTNSYTPNNAIEKNNNGN----CNRSNNNTQNYIKLLQSNV 99
Query: 80 NSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN----EYTIINCMKNNSG 135
             T +N I N
                         ++ * KN N I+N * + N + NN
Sbjct: 100 NFNKIKTPQENTIINLNKINQLHN------KNQICSNRINNLCNYDEQLCNILNNNEK 151
Query: 136 WKISIRGNRIIWTLIDINGKTKSVFFEYN--IREDISEYINRWFFVTITNNLNNAKIYIN 193
          K + GN I T N T +++ N I + S+YIN+ ++I N +N + + N
Sbjct: 152 DKKKLHGNNNIITHNHQNNITSTLYNYDNSCIENNQSDYINK---LSIKNKVNTSNTFYN 208
Query: 194 ----GKLESNTDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTELSOSNIEERY 249
             G L
                  IK ÷
                            N + DG+ F
                                                + 5
Sbjct: 209 IDQFGLLNKKKKIKSLE----NLKSYISNDGESFNNSFTIKPFNSYNKSTMKVKNILSNE 264
Query: 250 KIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS-KYI 308
               + K+F N + N E+Y GN N+ + D
Sbjct: 265 KTILCRKNCKNFILNKRI-NLEHYNSKKGNSNNNDMNESDVVKNYKQDYGNNNNNSNNYY 323
Query: 309 NYRDLYIGEKFIIRRKSNSQSINDD-IVRKEDYIYLDFFN 347
           A D AI + +M +DD ++K ++IA L+M
Sbjct: 324 YYSDNYINDDDNNNYYNNYYYDDDDGDIKKGEHIY--FYN 361
tr Q7WRP2
               Botulinum neurotoxin type E (Fragment) [bont/E]
                                                                      71 AA
```

Q7WRP2 CLOBU [Clostridium

butyricum]

align

```
Score = 45.1 bits (105), Expect = 0.003
Identities = 29/76 (38%), Positives = 42/76 (55%), Gaps = 7/76 (9%)
Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325
          L+Y+KEYY+ N N++I + DS TS NS + LY GK T+R +
Sbjct: 2 LLYDKEYYLLNVLKPNNFINRRTDS-----TLSINNIRSTILLANRLYSGIKVKIQRVN 55
Query: 326 NSQSINDDIVRKEDYI 341
         NS S ND++VR +D +
Sbjct: 56 NS-STNDNLVRNDDRV 70
tr Q6DN58
               COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (Yeast)] 396 AA
   Q6DN58 KLULA
                                                                    align
 Score = 44.7 bits (104), Expect = 0.004
Identities = 65/257 (25%), Positives = 105/257 (40%), Gaps = 47/257 (18%)
Query: 106 IRIPKYKNDGIQ-----NYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKS 158
          I+I KYK+ +O N I+N +K+ I+I N +IW + DI
sbjct: 152 IQINKYKSKYLQFRLIIKLNNNKENINILNNIKHYLKGNININNNYVIWIINDIK---- 206
Query: 159 VFFEYNIREDISEYINRWFFVTITNNLNNAKI----YI---NGKLESNTDIKDIREVIAN 211
              NI ++ + M++ +TI L A I YI N L N +KD
Sbjct: 207 ----NI-NNLIKLFNKYPLITINKKLQLAFIKSIYYIYKNNRNLAINLYLKDRNN--KY 258
Query: 212 GEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKI-QSYSEYLKDFWGNPLMYNK 270
             ++K DI+ T+ + YFS N + I I +Y+ + W + NK
Sbjct: 259 NPNLYKYYKDINYTK---INYFSPANFHKKFAGININININNNYNHNYINVWFLGFIENK 315
Query: 271 EYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSI 330
           ++ NNS++ D +EL+++N +KI ++YIE+ N I
Sbjct: 316 GKFIIRKNNNNSFLFYINDKHLIEFL-KNYFNIKNKLIYKNNIYILEVY-----NKYYI 368
Query: 331 NDDIVRKEDYIYLDFFN 347
             I++ FEN
Sbjct: 369 N-----IFIKFFN 376
              Hypothetical protein [PFL0360c] [Plasmodium falciparum
   Q8I5X3 PLAF7 (isolate 3D7)]
                                                                     AΑ
                                                                     align
 Score = 43.9 \text{ bits } (102), \text{ Expect} = 0.008
Identities = 77/364 (21%), Positives = 136/364 (37%), Gaps = 61/364 (16%)
           NDTILIEMFNKYNSEXXXXXXXXXXXYKDN--NLIDLSGYGA-KVEVYDGVELNDKNQFKL 75
           N I I YN + D+ N + GY V + + N K
Sbjct: 2276 NYDIFISQHKLYNDVTSMDKKEFNKQSDHIFNNYHIDGYNVDNVRSSNHISNNSIIINKR 2335
           TSSANSKIRVTQ----NQNIIFNSVFLDFSVSFWIRIPKYKNDGIQ-----NYIHN 122
Query: 76
                        N+N+TFN+ ++ ++ + K N+
Sbjct: 2336 QMMSNNKIVINNHHISNKNMIFNNNIINNNIIMYNK--KKSNNSSSSCCINTMHGNNNNN 2393
```

```
.Score = 45.1 bits (105), Expect = 0.003
Identities = 29/76 (38%), Positives = 42/76 (55%), Gaps = 7/76 (9%)
Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325
          L+Y+KRYY+ N N++X + DS TS NS + LY G K X+R +
Sbjct: 2 LLYDKEYYLLNVLKPNNFINRRTDS-----TLSINNIRSTILLANRLYSGIKVKIQRVN 55
Query: 326 NSQSINDDIVRKEDYI 341
         NS S ND++VR +D +
Sbjct: 56 NS-STNDNLVRNDDRV 70
tr <u>Q6DN58</u>
               COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (Yeast)] 396 AA
   Q6DN58 KLULA
                                                                    align
 Score = 44.7 bits (104), Expect = 0.004
 Identities = 65/257 (25%), Positives = 105/257 (40%), Gaps = 47/257 (18%)
Query: 106 IRIPKYKNDGIQ-----NYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKS 158
          I+I KYK+ +Q N I+N +K+ I+I N +IW + DI
Sbjct: 152 IQINKYKSKYLQFRLIIKLNNNKENINILNNIKHYLKGNININNNYVIWIINDIK----- 206
Query: 159 VFFEYNIREDISEYINRWFFVTITNNLNNAKI----YI---NGKLESNTDIKDIREVIAN 211
              NI ++ + M++ +TI L A I YI N L N +KD
Sbjct: 207 ----NI-NNLIKLFNKYPLITINKKLQLAFIKSIYYIYKNNRNLAINLYLKDRNN--KY 258
Query: 212 GEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKI-QSYSEYLKDFWGNPLMYNK 270
             ++K DI+ T+ + YFS N + I I +Y+ + W + NK
Sbjct: 259 NPNLYKYYKDINYTK---INYFSPANFHKKFAGININININNNYNHNYINVWFLGFIENK 315
Query: 271 EYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSI 330
           ++ NNS++ D + E L ++ +N +K I ++YI E + N I
Sbjct: 316 GKFIIRKNNNNSFLFYINDKHLIEFL-KNYFNIKNKLIYKNNIYILEVY-----NKYYI 368
Query: 331 NDDIVRKEDYIYLDFFN 347
             I++ FEN
Sbjct: 369 N-----IFIKFFN 376
              Hypothetical protein [PFL0360c] [Plasmodium falciparum
tr <u>Q8</u>I5X3
                                                                     2723
                                                                     AΑ
   Q8I5X3 PLAF7 (isolate 3D7)]
                                                                     align
 Score = 43.9 bits (102), Expect = 0.008
 Identities = 77/364 (21%), Positives = 136/364 (37%), Gaps = 61/364 (16%)
           NDTILIEMFNKYNSEXXXXXXXXXXXXXXKYKDN--NLIDLSGYGA-KVEVYDGVELNDKNQFKL 75
           N II YN + D+ N + GY V + + N K
Sbjct: 2276 NYDIFISQHKLYNDVTSMDKKEFNKQSDHIFNNYHIDGYNVDNVRSSNHISNNSIIINKR 2335
           TSSANSKIRVTQ----NQNIIFNSVFLDFSVSFWIRIPKYKNDGIQ-----NYIHN 122
Query: 76
              +N+KI + N+N+IFN+ ++ ++ + K N+
Sbjct: 2336 QMMSNNKIVINNHHISNKNMIFNNNIINNNIIMYNK--KKSNNSSSSCCINTMHGNNNNN 2393
```

```
Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDIN---GKTKSVFFEYNIREDISEYINRWFFV 179
               N ++N + KI I+ N I+ + N S F N E+S + + V
Sbjct: 2394 NFQCSNILRNMTNQKIDIKDNMILKKISTNNCEMNNLNSCSFLSNSSENGSYKTDEFLNV 2453
Query: 180 TITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
                +M+ I + E M +K N +I
                                               DI+
Sbjct: 2454 NEKYRINDLNILHSNNKEVNNILKGHNIKHNNNKI----NDIN-----ILHSNN 2498
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLK------KDS 290
              Sbjct: 2499 KEVNNILKSHNIKHNNNKINDI--NILHSHNEFYNIHTNNHKSDLKCVGGHITNDRYENS 2556
Query: 291 PVGEILTRSKYN------QNSKYI---NYRDLYIGEKFIIRRKSNSQSINDDIVR 336
            + +1 T K N
                                +N KY+ N+ ++Y+GE I+ N
Sbjct: 2557 ILSQIKTHEKENIRQIKHTNIEEENKKYVLPVNHNEIYLGEHNKIKSDKNETQDNDTIGK 2616
Query: 337 KEDY 340
Sbjct: 2617 KIIY 2620
 Score = 34.3 bits (77), Expect = 6.0
 Identities = 65/299 (21%), Positives = 120/299 (39%), Gaps = 36/299 (12%)
           NKYNSEXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGVELNDKNOFKLTSSANSKIRVTO 87
Query: 28
           N + WS RY + + + T + Y + Y + N + + + + K + TQ
Sbjct: 1271 NNHNSNNNNHINRDRYINHHNIISNEYIRQQIKYTNINFNNHKNDSINENVRNKSTITQ 1330
Query: 88 NQNIIFNS-----VFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKIS 139
              + +N+ D + T Y N+ ++++N + N
Sbjct: 1331 VNGLNYNTNEKDKEKINHNDNHIHTKRIIRNYSNNLDMHFMNNNIHLDNNNNNNNNNNNN 1390
Query: 140 IRG-NRIIWTLI-----DINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIY-I 192
               N \perp W \perp \qquad \qquad K + F - N + I \qquad ++ \qquad N + N + IY \perp
Sbjct: 1391 NNNCNYIRWENIFPYCNSCKNKYANKFEINNFDNNIMNKYEKYECTCCGNKIRNEEIYNI 1450
Query: 193 NGKLESNTDIKDIREV--IANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
            GK+ S ++++I + I N + I + + + + WM F ++N E YK
Sbjct: 1451 LGKVTSE-NLRNIYKSNRINNTDNILRYNRENE-----WMSSFF-----FKENNNREIYK 1499
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYIN 309
            + Y EY DF+ N + E M N +N+ +K K + E +T++
Sbjct: 1500 -EEYDEYKNDFFLN--IKEGEKSMLNNIFRNNSLKEKLINE--ENITKT---NNNVYVN 1550
tr
     Q7RP92
                        Clp [PY01567] [Plasmodium yoelii yoelii] 518 AA
     Q7RP92 PLAYO
                                                               align
 Score = 43.5 bits (101), Expect = 0.010
 Identities = 65/268 (24%), Positives = 107/268 (39%), Gaps = 45/268 (16%)
Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
          FS+ + I K KN N IN +N + ISI N I++ K +
Sbjct: 78 FSIKLLLDIKKVKNI-----NSLEKINMNENKIKYIISI--NLILFCY-----KII 121
Query: 160 FFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREV----- 208
```

```
Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDIN---GKTKSVFFEYNIREDISEYINRWFFV 179
              N ++N + KI I+ N I+ + N S F N E+ S + + V
Sbjct: 2394 NFQCSNILRNMTNQKIDIKDNMILKKISTNNCEMNNLNSCSFLSNSSENGSYKTDEFLNV 2453
Query: 180 TITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
               +M+ I + E M +K N +I
                                              DI+
Sbjct: 2454 NEKYRINDLNILHSNNKEVNNILKGHNIKHNNNKI----NDIN-----ILHSNN 2498
Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLK-----KDS 290
             +NT + + T+ + + D N L + E+Y + N S +K
Sbict: 2499 KEVNNILKSHNIKHNNNKINDI--NILHSHNEFYNIHTNNHKSDLKCVGGHITNDRYENS 2556
Ouery: 291 PVGEILTRSKYN------QNSKYI---NYRDLYIGEKFIIRRKSNSQSINDDIVR 336
           + +1 T K N +N KY+ N+ ++Y+GE I+ N ND I +
Sbjct: 2557 ILSQIKTHEKENIRQIKHTNIEEENKKYVLPVNHNEIYLGEHNKIKSDKNETQDNDTIGK 2616
Query: 337 KEDY 340
Sbjct: 2617 KIIY 2620
 Score = 34.3 bits (77), Expect = 6.0
 Identities = 65/299 (21%), Positives = 120/299 (39%), Gaps = 36/299 (12%)
          NKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQ 87
Query: 28
          Sbjct: 1271 NNHNSNNNNHHINRDRYINHHNIISNEYIRQQIKYTNINFNNHKNDSINENVRNKSTITQ 1330
Query: 88 NQNIIFNS-----VFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKIS 139
             + +N+ D + T Y N+ ++++N + N NN+
Sbjct: 1331 VNGLNYNTNEKDKEKINHNDNHIHTKRIIRNYSNNLDMHFMNNNIHLDNNNNNNNNNNN 1390
Query: 140 IRG-NRIIWTLI-----DINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIY-I 192
              NIWI K + F N +I ++
                                                      N + N +IY I
Sbjct: 1391 NNNCNYIRWENIFPYCNSCKNKYANKFEINNFDNNIMNKYEKYECTCCGNKIRNEEIYNI 1450
Query: 193 NGKLESNTDIKDIREV--IANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK 250
           GK+ S ++++I + I N + I + + + + WM F ++N E YK
Sbjct: 1451 LGKVTSE-NLRNIYKSNRINNTDNILRYNRENE----WMSSFF----FKENNNREIYK 1499
Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYIN 309
           + Y EY DE+ N + E M N +N+ +K K + E +T++ N+ Y+N
Sbjct: 1500 -EEYDEYKNDFFLN--IKEGEKSMLNNIFRNNSLKEKLINE--ENITKT---NNNVYVN 1550
tr
    Q7RP92
                       Clp [PY01567] [Plasmodium yoelii yoelii] 518 AA
     Q7RP92 PLAYO
                                                             align
 Score = 43.5 bits (101), Expect = 0.010
 Identities = 65/268 (24%), Positives = 107/268 (39%), Gaps = 45/268 (16%)
Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
         FS+ + I K KN N IN +N + ISI N I++ K +
Sbjct: 78 FSIKLLLDIKKVKNI-----NSLEKINMNENKIKYIISI--NLILFCY-----KII 121
Query: 160 FFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREV----- 208
```

```
+ YN+ S +T R+ V+ NN IN +
                                                ++7 ++
Sbjct: 122 KYIYNLFLSYSYFIFRFSSVSNLNNKEFLLCIINNNIFLKKTFENIYDIYLNYKELFNFY 181
Query: 209 IANGEIIFKLDGDIDRTQFIWMKYFSIF--NTELSQSNIEER--YKIQSYSEYLKDFWGN 264
          I EILE++D DI + KY + E NEE+ +N++++
                                                  K+ + Y N
Sbjct: 182 IXQKEIIFEMD-DIKKNSIFQKKYMNTFNTNTEIYPTNLDDKNINKVDNNMCYEDKVIKN 240
Query: 265 PLM---YNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFII 321
               NKEYN + N +K EL K ++ + N L
Sbjct: 241 KIFEDATNKEKY--NKCDDNDSVKNNSSEYKDEFLINKKTHELDEKKNTLKLSKNVKFL- 297
Query: 322 RRKSNSQSINDDIVRKEDYIYLDFFNLN 349
                +N + K ++Y+D F +N
Sbjct: 298 -----CVNKISIFKNMHLYIDKFYIN 318
tr Q7RDL0
               Hypothetical protein [PY05412] [Plasmodium yoelii
                                                                     834
   Q7RDL0_PLAYO yoelii] .
                                                                     AA
                                                                     align
 Score = 43.5 bits (101), Expect = 0.010
 Identities = 58/243 (23%), Positives = 108/243 (43%), Gaps = 36/243 (14%)
Query: 106 IRIPKYKNDGIQNYIHN-EYTIIN-----CMKNNSGWKISIRGNRIIWTLIDINGKTK 157
          THIRY DI I TYTH N CKNN S TITT THE TE
Sbjct: 283 IKIQKYEEDKIGEIICRLKYSLDNVNNGIEICKKNNFHMNFSELKEKIIKSLNFFEHENK 342
Query: 158 SVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
          +++EE D + + \Lambda + N++ ++IXI K + D+K + M I ++
Sbjct: 343 NIYFEVIPTYDNLDKLKGTEVVKV-KNIDISEIYI--KKNISNDLKLLFNKQAQ-NIYYQ 398
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK-----IQSYSEYLKDFWGNPLMY 268
          +G++ + ++ K F + N + NI R I +Y+* +KD++ + Y
Sbjct: 399 YNGELTQLYNLFEKNFIVLNDQFKIMNISNRKNIISSLNNAIINTYNK-IKDYYKPAIYY 457
Query: 269 NKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQ 328
         N MAN ++++I++NN++YN++KI
Sbjct: 458 NN----LNALN-----NVETHLQDIIIQIEANLNTEYKNNFEF---QKKFINVGINQE 503
Query: 329 SIN 331
         SIM
Sbjct: 504 SIN 506
tr Q6LFF0
              Hypothetical protein [PFF0575c] [Plasmodium falciparum
                                                                    3248
   Q6LFF0 PLAF7 (isolate 3D7)]
                                                                    AΑ
                                                                    align
Score = 43.5 bits (101), Expect = 0.010
Identities = 52/241 (21%), Positives = 99/241 (40%), Gaps = 35/241 (14%)
Query: 113 NDGIQNYIHNEYTII-----NCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIR 166
          N I N ++N TI+ + + NN S N + + ++
Sbjct: 1585 NQNIHNRMNNTNTIVQNNVRSSILLNNKNNSNSSNNNNLPYDKENVTNIKYDLLNNKNVH 1644
```

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+ YN+ S +X R+ V+ NN IN + ++X ++
Sbjct: 122 KYIYNLFLSYSYFIFRFSSVSNLNNKEFLLCIINNNIFLKKTFENIYDIYLNYKELFNFY 181
Query: 209 IANGEIIFKLDGDIDRTQFIWMKYFSIF--NTELSQSNIEER--YKIQSYSEYLKDFWGN 264
          I BILE++D DI + KY + E MEE+ +N++++ K+ + E
Sbjct: 182 IXQKEIIFEMD-DIKKNSIFQKKYMNTFNTNTEÍYPTNLDDKNINKVDNNMCYEDKVIKN 240
Query: 265 PLM---YNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFII 321
          + NKE Y N + N +K E L K ++ + N L KE+
Sbjct: 241 KIFEDATNKEKY--NKCDDNDSVKNNSSEYKDEFLINKKTHELDEKKNTLKLSKNVKFL- 297
Query: 322 RRKSNSQSINDDIVRKEDYIYLDFFNLN 349
                *N + K ++Y+D F +N
Sbjct: 298 -----CVNKISIFKNMHLYIDKFYIN 318
tr Q7RDL0
              Hypothetical protein [PY05412] [Plasmodium yoelii
                                                                     834
   Q7RDL0_PLAYO yoelii]
                                                                    AΑ
                                                                    align
Score = 43.5 bits (101), Expect = 0.010
Identities = 58/243 (23%), Positives = 108/243 (43%), Gaps = 36/243 (14%)
Query: 106 IRIPKYKNDGIQNYIHN-EYTIIN-----CMKNNSGWKISIRGNRIIWTLIDINGKTK 157
          I+I KY+ D I I +Y++ M C KNN S +II +L + K
Sbjct: 283 IKIQKYEEDKIGEIICRLKYSLDNVNNGIEICKKNNFHMNFSELKEKIIKSLNFFEHENK 342
Query: 158 SVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
          +++FE D + + V + N++ ++IYI K + D+K + A I ++
Sbjct: 343 NIYFEVIPTYDNLDKLKGTEVVKV-KNIDISEIYI--KKNISNDLKLLFNKQAQ-NIYYQ 398
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYK-----IQSYSEYLKDFWGNPLMY 268
          +G++ + ++ K F + N + NI R I +Y++ +KD++ + Y
Sbjct: 399 YNGELTQLYNLFEKNFIVLNDQFKIMNISNRKNIISSLNNAIINTYNK-IKDYYKPAIYY 457
Query: 269 NKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQ 328
         N = NX N ++++I+++N N++Y N + +K I
Sbjct: 458 NN----LNALN-----NVETHLQDIIIQIEANLNTEYKNNFEF---QKKFINVGINQE 503
Query: 329 SIN 331
         SIN
Sbjct: 504 SIN 506
tr Q6LFF0
             Hypothetical protein [PFF0575c] [Plasmodium falciparum
                                                                    3248
   Q6LFF0 PLAF7 (isolate 3D7)]
                                                                    <u>align</u>
Score = 43.5 bits (101), Expect = 0.010
Identities = 52/241 (21%), Positives = 99/241 (40%), Gaps = 35/241 (14%)
Query: 113 NDGIQNYIHNEYTII-----NCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIR 166
          N IN ++N TI+ + + NN S N + + ++ +
Sbjct: 1585 NQNIHNRMNNTNTIVQNNVRSSILLNNKNNSNSSNNNNLPYDKENVTNIKYDLLNNKNVH 1644
```

```
Query: 167 EDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG----D 221
                F+ NLNN+ + +N + N +DI + NG+I+ +G
Sbjct: 1645 NNIP-----FIGTKINLNNSLVQLNNNMNKNILSEDINK---NGDILNSFNGNALPIN 1694
Query: 222 IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKD-FWGNPLMYNKEYYMFNAGNK 280
           DR ++ +S NT ++++ + ++ S +L F N + NK
Sbjct: 1695 YDRNEY--ASSYSEKNTNINETYMNSMINSKNNSIHLNQMFTKNTITSNK-----NSSNE 1747
Query: 281 NSYIKLKKDSPVGEI--LTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKE 338
             + KK + I L + N N +IN +I ++R SN D + K+
Sbjct: 1748 KQIMNRKKLTKTQNINNLKATDINSNINFIN----HINNNSDVKRMSNFNIHRDGMYLKD 1803
Query: 339 D 339
Sbjct: 1804 E 1804
                                                                     595
tr Q8IDG1
               Hypothetical protein PF13_0283 [PF13_0283] [Plasmodium
   Q8IDG1_PLAF7 falciparum
                                                                     AΑ
               (isolate 3D7)]
                                                                     <u>align</u>
 Score = 43.1 bits (100), Expect = 0.013
 Identities = 42/170 (24%), Positives = 73/170 (42%), Gaps = 33/170 (19%)
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF------ 233
          NN K YIN K N + DI+++ N I + +++ +
                                                  EY +
Sbjct: 112 NNNKCYINVKNSFNNERNDIKQMQKNSYINY----LNKLKKNGNKYYDTCQNNIYGKET 166
Query: 234 ---SIFNTELSQSNIEERYKIQSYSEYL-----KDFWG--NPLMYNKEYYMFNAGNKNS 282
            +T+T+SS+++S++Y + +G N + YN + + N
Sbjct: 167 QVDNIYRTNMSTSSKKYMNNMNSFGKYTINNIIKNNIYGTNNNINYNIQQFNINCNEKNC 226
Query: 283 YIKLKKDSPVGEILTRSKYNQNSKYINY--RDLYIGEKFIIRRKSNSQSI 330
          + KL K G I T S N + Y Y + + I K + I++K + I
Sbjct: 227 FHKLNKS---GLIKTYSFNNYKNSYATYKQKQIIIKNKSLIQKKGENNYI 273
tr Q8I3X5
               Hypothetical protein PFE0655w [PFE0655w] [Plasmodium
                                                                    2763
   Q8I3X5 PLAF7 falciparum
               (isolate 3D7)]
                                                                    align
Score = 43.1 bits (100), Expect = 0.013
Identities = 69/338 (20%), Positives = 135/338 (39%), Gaps = 43/338 (12%)
Query: 12
          FDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGVELNDKN 71
           +D +IY
                  IL++ ++N +
                                         +NN + Y + VY +++N
Sbjct: 1744 YDENIYNGSYILLD---EHNFKEPTNKMNKKNNNNNNKKKNVYYNCLVVYPYIDIN--- 1797
Query: 72
          QFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFW-----IRIPKYKNDGIQNYIHNE 123
            Sbjct: 1798 --KITTNISDDKNVSKELFEKDIMNNYYINYPILFLSNYKGKLYIHPLNKEKLQQSYHNN 1855
Query: 124 YTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN 183
                 KNN++I NI*++DIG K+ *+ E IS
Sbjct: 1856 KEEKEPNKNNNNYIIHYAHNNILYNIKDIYGHIKGL-HKIDQNEFISFSNNKFQIF---- 1910
```

```
Query: 167 EDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG----D 221
                 F+ NLNN+ + +N + N +DI + NG+I+ +G
Sbjct: 1645 NNIP-----FIGTKINLNNSLVQLNNNMNKNILSEDINK---NGDILNSFNGNALPIN 1694
Query: 222 IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKD-FWGNPLMYNKEYYMFNAGNK 280
            DR ++ +S NT ++++ + + + S +L F N + NK
Sbjct: 1695 YDRNEY--ASSYSEKNTNINETYMNSMINSKNNSIHLNOMFTKNTITSNK-----NSSNE 1747
Query: 281 NSYIKLKKDSPVGEI--LTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKE 338
              + KK +
                       I L + N N +IN +I
                                                   ++R SN
Sbjct: 1748 KQIMNRKKLTKTQNINNLKATDINSNINFIN----HINNNSDVKRMSNFNIHRDGMYLKD 1803
Query: 339 D 339
Sbjct: 1804 E 1804
tr Q8IDG1
                Hypothetical protein PF13_0283 [PF13_0283] [Plasmodium
                                                                       595
   Q8IDG1_PLAF7 falciparum
                                                                       AΑ
                (isolate 3D7)]
                                                                       align
 Score = 43.1 bits (100), Expect = 0.013
 Identities = 42/170 (24%), Positives = 73/170 (42%), Gaps = 33/170 (19%)
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF----- 233
          NN K YIN K
                     N + DI+++ N I +
                                            4-4-4-
                                                    \mathbb{R}^{N}
Sbjct: 112 NNNKCYINVKNSFNNERNDIKQMQKNSYINY----LNKLKKNGNKYYDTCQNNIYGKET 166
Query: 234 ---SIFNTELSQSNIEERYKIQSYSEYL-----KDFWG--NPLMYNKEYYMFNAGNKNS 282
             +II+III+SS++++S++III + +GIII+III+III
Sbjct: 167 QVDNIYRTNMSTSSKKYMNNMNSFGKYTINNIIKNNIYGTNNNINYNIQQFNINCNEKNC 226
Query: 283 YIKLKKDSPVGEILTRSKYNQNSKYINY--RDLYIGEKFIIRRKSNSQSI 330
          + KL K G I T S N + Y Y + + T K + T++K + T
Sbjct: 227 FHKLNKS---GLIKTYSFNNYKNSYATYKQKQIIIKNKSLIQKKGENNYI 273
tr Q8I3X5
                Hypothetical protein PFE0655w [PFE0655w] [Plasmodium
                                                                      2763
   Q8I3X5_PLAF7 falciparum
                                                                      AΑ
                (isolate 3D7)]
                                                                      <u>align</u>
 Score = 43.1 bits (100), Expect = 0.013
 Identities = 69/338 (20%), Positives = 135/338 (39%), Gaps = 43/338 (12%)
           FDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKN 71
Query: 12
           +D +IY
                  IL++ ++N +
                                           +NN
                                                  ÷ Ÿ
                                                       + VY +++N
Sbjct: 1744 YDENIYNGSYILLD---EHNFKEPTNKMNKKNNNNNNKKKNVYYNCLVVYPYIDIN--- 1797
Query: 72
           QFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFW-----IRIPKYKNDGIQNYIHNE 123
             K+T++ + V++ + I N+ ++++ + F * I
Sbjct: 1798 --KITTNISDDKNVSKELFEKDIMNNYYINYPILFLSNYKGKLYIHPLNKEKLQQSYHNN 1855
Query: 124 YTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN 183
                 KNN++I NI*++DIGK+ ++EIS
Sbjct: 1856 KEEKEPNKNNNNYIIHYAHNNILYNIKDIYGHIKGL-HKIDQNEFISFSNNKFQIF---- 1910
```

```
Query: 184 NLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQS 243
           N+N+ K N + +T+ + II+ ++ N ++
Sbjct: 1911 NINDYK--YNSVMPKSTQVNIRSDFFLTSTIINEQSNESNN------NNNNNN 1956
Query: 244 NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQ 303
           N I + K++GN+N Y + G+MSY S +I+ SK
Sbjct: 1957 NNNNNNNINNNGN--KNNYGNKIHLNNPYGDTHIGHINSYSNPNHISIQNDIIFFSK--- 2011
Query: 304 NSKYINYRDLYIGEKFIIRRKSNSOSINDDIVRKEDYI 341
           NS IN L + F ++ + I+ + K+DY+
Sbjct: 2012 NSNLIN---LSFNDSFATKKILSYPYIHKMCISKDDYV 2046
              Hypothetical protein [PY03232] [Plasmodium yoelii
   Q7RJM7_PLAYO yoelii]
                                                                   \Delta \Delta
                                                                   align
 Score = 43.1 bits (100), Expect = 0.013
 Identities = 64/305 (20%), Positives = 108/305 (34%), Gaps = 59/305 (19%)
Query: 14 LSIYTNDT----ILIEMFNKYNSEXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYD--GVEL 67
          LS Y +D · I+ Y S
                                        Y +WW++D S + +D
Sbjct: 328 LSFYCDDDDDNKIIFPPRQNYQSSTLQKLTGMLNYNNNNIVDKSALDRSMSYFDLRREKK 387
Query: 68 ND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYT 125
          ND KN K+ M IR N++ N++E
Sbjct: 388 NDIVKNYIKINKVRNGNIR---NEDNATNNIF-------NNYIHKD-- 423
Query: 126 IINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNL 185
                   KI + G L +++ + +YN D IR + IN+
Sbjct: 424 -----ENRKIYVHGEN---DLNNVDMHRNAFDHDYNKNYDTMHNIRRSTNI-IDNLV 471
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTOFIWMKYFSIFNTELSOSNI 245
          +N + + M + + M + + M + + M
Sbjct: 472 HNRLVYNNNHIFNNNENINILNKITNPDTVYPLD-----FRSNNTHDGICNN 518
Query: 246 EERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNONS 305
           +\lambda \lambda + + \lambda + +K +M M ++ +K E+F
Sbjct: 519 IGKY--DRYNNFNYKTIDNKYIYDKNNFMHENENYVNFSYIKNIEKFKELLINIATDNLK 576
Query: 306 KYINY 310
          +Y+Y
Sbjct: 577 EYVKY 581
tr Q9EMF0
               AMV256 [AMV256] [Amsacta moorei entomopoxvirus (AmEPV)] 609 AA
   Q9EMF0 AMEPV
                                                                   align
Score = 42.4 bits (98), Expect = 0.022
Identities = 87/373 (23%), Positives = 148/373 (39%), Gaps = 83/373 (22%)
Query: 17 YTNDTILIEMFN-KYNSEXXXXXXXXXXXXRYKDNNLIDLSGYGA--KVEVYDGVELNDKNQF 73
         YN +LT + + K S
                            YK N + Y K+E D V LN+
```

```
Query: 184 NLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQS 243
          N+N+ K N + +T + + II + + + N + +
Sbjct: 1911 NINDYK--YNSVMPKSTQVNIRSDFFLTSTIINEQSNESNN------NNNNNN 1956
Query: 244 NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQ 303
          N I + K++GN+NY+G+NSY S +I+ SK
sbjct: 1957 NNNNNNNINNNGN--KNNYGNKIHLNNPYGDTHIGHINSYSNPNHISIQNDIIFFSK--- 2011
Query: 304 NSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYI 341
          NS IN L + F ++ + I+ + K+DY+
Sbjct: 2012 NSNLIN---LSFNDSFATKKILSYPYIHKMCISKDDYV 2046
              Hypothetical protein [PY03232] [Plasmodium yoelii
                                                                1652
tr Q7RJM7
   Q7RJM7 PLAYO yoelii]
                                                                AA
                                                                align
Score = 43.1 bits (100), Expect = 0.013
Identities = 64/305 (20%), Positives = 108/305 (34%), Gaps = 59/305 (19%)
LS Y +D
                 I+ \qquad Y S \qquad \qquad Y + NN++D S \qquad + \qquad + D
Sbjct: 328 LSFYCDDDDDNKIIFPPRQNYQSSTLQKLTGMLNYNNNNIVDKSALDRSMSYFDLRREKK 387
Query: 68 ND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYT 125
         ND KN K+ N IR N++ N++F
Sbjct: 388 NDIVKNYIKINKVRNGNIR---NEDNATNNIF------NYIHKD-- 423
Query: 126 IINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNL 185
                   KI + G L +++ + +YN D IR + IN+
Sbjct: 424 -----ENRKIYVHGEN---DLNNVDMHRNAFDHDYNKNYDTMHNIRRSTNI-IDNLV 471
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNI 245
         Sbjct: 472 HNRLVYNNNHIFNNNENINILNKITNPDTVYPLD-----FRSNNTHDGICNN 518
Query: 246 EERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS 305
               X+ + N +X+K +W N ++ +K
                                                  E+1.
Sbjct: 519 IGKY--DRYNNFNYKTIDNKYIYDKNNFMHENENYVNFSYIKNIEKFKELLINIATDNLK 576
Query: 306 KYINY 310
         *X + X
Sbjct: 577 EYVKY 581
tr Q9EMF0
              AMV256 [AMV256] [Amsacta moorei entomopoxvirus (AmEPV)] 609 AA
   Q9EMF0 AMEPV
                                                                align
 Score = 42.4 bits (98), Expect = 0.022
 Identities = 87/373 (23%), Positives = 148/373 (39%), Gaps = 83/373 (22%)
Query: 17 YTNDTILIEMFN-KYNSEXXXXXXXXXXXYKDNNLIDLSGYGA--KVEVYDGVELNDKNQF 73
                                 YK N + Y K+E D V LN*
         YN +LT + + K S
```

```
Sbjct: 255 YYNKLVLINILSDKLLSLTIYFLTSEYMYKSLNYFETIDYSKIKKLEFDDYVILNE--YF 312
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVS-----FWIRIPKYKNDGIQNYIHNEYTI 126
          + + N+ . N+ + + ++D+ ++ E+++IP
Sbjct: 313 DIINIYNNIKSNNINKYYSYYNKYIDYIINSSTDINKFFLQIPN-----QLYLNNEFDI 366
Query: 127 INCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN-NL 185
                     + + + I+ N K K NI
Sbjct: 367 NNIPV-----FKAETLFNSKINTNNKNKIT---NINN-----IEILNFNV 403
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ-----FIWMKYFSIFN 237
         NN ++N +E +IK+ +I N + I+K D +I + + KYF I+
Sbjct: 404 NNMIFFMN-VIEDKFEIKNNEIIIKNTKNIYKSDNNICVLNNNYNYPKIYFYYKYFIIYF 462
Query: 238 TELSQSNIEERYKIQSYSEYL-----KDFWGNPLMYNKE-----YYMFN 276
               ML++ + X X +E M L+ MK+
Sbjct: 463 FSNIFLNIDDAIEYVKYKPYFNLLNNINVENNFNTNILINNKKININTNHDFITALYIYN 522
Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
           NKN YI + + + + + LL R + IN+ + + FII K + I+ +R
Sbjct: 523 CNNKNCYIHM---ATISDIL-RDLGLIYTPIINFENNLV-YLFIITNKPHETEIH---LR 574
Query: 337 KEDYIYLDFFNLN 349
         K I D FN+N
Sbjct: 575 K---ILNDKFNVN 584
```

Hypothetical protein [PF11\_0168] [Plasmodium falciparum 2966 Q8IIK5 PLAF7 (isolate 3D7)] align Score = 42.0 bits (97), Expect = 0.029Identities = 91/406 (22%), Positives = 160/406 (38%), Gaps = 76/406 (18%) Query: 44 YKDNNLIDLSGYGAKVEVYDGVELNDKNQFK---LTSSANSKI----RVTQNQNIIFNS 95 Y+++N + + + K +Y+ NDK+ +K D S+++ K+ ++ +N+N+D + Sbjct: 1342 YQNSNCSNKNSFNNKDHIYNNTMNNDKDTYKYGTLNSNSDHKMNICDEKIKKNKNMINDİ 1401 Query: 96 VFLDFSVSFWIRIPKYKNDGIQNY-IHNEYTIINCMKNNSGWKISIRG----NRIIWTL 149 ++ I N I NY I+ T N N+ KI + N I T Sbjct: 1402 NIQNITDKHVI-----NKNIINYKINENKTENNIPLVNNKNKILVNNNIHTYNNIHMTN 1455 Query: 150 IDINGKTKSVFFEYNIREDI-----SEYINRWFFVTITNNLNNAKIYINGKLESNT--D 201 I+ + K+ F EY E + S+ IN T+ NML K K+E+N Sbjct: 1456 INALHEKKTKFGEYKYFEKLFFDCLKSKIINE--IKTLDNNLKKKK--KKKKIETNKLFS 1511 Query: 202 IKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQ----- 252 T++ +T N ++ + + + + + + + + + + T + + T Sbjct: 1512 IQNTINIIKNYSFLYPSKNNNNEQKKKKNSQSSTESSGTTNNNIDSKNDIHMNKKLEDTS 1571 Query: 253 ----SYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYI 308 +YS K+ WG + FN K+ KD+ V + Sbjct: 1572 HVMPNYSVGEKNSWGKEKLKKLMDIYFNE-----KVLKDTNVSNNMNECISNGNIKQM 1624 Query: 309 NYRDLYIGEKFIIRRKSNSQ-SINDDI---VRKEDYIYLDFFNLNQEWRVYTXXXXXXXX 364 + + I EK N +IND+I \* + + Y\* F + E

```
Sbjct: 255 YYNKLVLINILSDKLLSLTIYFLTSEYMYKSLNYFETIDYSKIKKLEFDDYVILNE--YF 312
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVS-----FWIRIPKYKNDGIQNYIHNEYTI 126
                      N+ + + ++D+ ++
                                             F+++IP
Sbjct: 313 DIINIYNNIKSNNINKYYSYYNKYIDYIINSSTDINKFFLQIPN-----QLYLNNEFDI 366
Query: 127 INCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN-NL 185
                       + + + I+ N K K NI
Sbjct: 367 NNIPV-----FKAETLFNSKINTNNKNKIT----NINN-----IEILNFNV 403
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ-----FIWMKYFSIFN 237
          NN \quad ++N \quad +E \quad +IK+ \quad +I \quad N \ + \ I+K \quad D \ +I \qquad \qquad + \ + \quad +KYF \quad I+
Sbjct: 404 NNMIFFMN-VIEDKFEIKNNEIIIKNTKNIYKSDNNICVLNNNYNYPKIYFYYKYFIIYF 462
Query: 238 TELSQSNIEERYKIQSYSEYL------KDFWGNPLMYNKE------YYMFN 276
                NI++ + X X +E N L+ NK+
Sbjct: 463 FSNIFLNIDDAIEYVKYKPYFNLLNNINVENNFNTNILINNKKININTNHDFITALYIYN 522
Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
            NKN YI + + + + IL R + IN+ + + FII K + I+ +R
Sbjct: 523 CNNKNCYIHM---ATISDIL-RDLGLIYTPIINFENNLV-YLFIITNKPHETEIH---LR 574
Query: 337 KEDYIYLDFFNLN 349
          K I D FN+N
Sbjct: 575 K---ILNDKFNVN 584
```

tr Q8IIK5 Hypothetical protein [PF11\_0168] [Plasmodium falciparum 2966 Q8IIK5\_PLAF7 (isolate 3D7)] AA align

Identities = 91/406 (22%), Positives = 160/406 (38%), Gaps = 76/406 (18%) YKDNNLIDLSGYGAKVEVYDGVELNDKNQFK---LTSSANSKI----RVTONONIIFNS 95 Y+++N + + + K +Y+ NDK+ +K 5 S+\*+ K+ ++ +N+N+I + Sbjct: 1342 YQNSNCSNKNSFNNKDHIYNNTMNNDKDTYKYGTLNSNSDHKMNICDEKIKKNKNMINDI 1401 Query: 96 VFLDFSVSFWIRIPKYKNDGIQNY-IHNEYTIINCMKNNSGWKISIRG----NRIIWTL 149 + + I N I NY I+ T N N+ KI + Sbjct: 1402 NIQNITDKHVI-----NKNIINYKINENKTENNIPLVNNKNKILVNNNIHTYNNIHMTN 1455 Query: 150 IDINGKTKSVFFEYNIREDI-----SEYINRWFFVTITNNLNNAKIYINGKLESNT--D 201 I + + K+ F EY E + S+ IN T+ NNL K K+E+N Sbjct: 1456 INALHEKKTKFGEYKYFEKLFFDCLKSKIINE--IKTLDNNLKKKK--KKKKIETNKLFS 1511 Query: 202 IKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQ----- 252 Sbjct: 1512 IQNTINIIKNYSFLYPSKNNNNEQKKKKNSQSSTESSGTTNNNIDSKNDIHMNKKLEDTS 1571 Query: 253 ----SYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYI 308 +YS K+ WG + FN K+ KD+ V + N N K + Sbjct: 1572 HVMPNYSVGEKNSWGKEKLKKLMDIYFNE-----KVLKDTNVSNNMNECISNGNIKQM 1624 Query: 309 NYRDLYIGEKFIIRRKSNSQ-SINDDI---VRKEDYIYLDFFNLNQEWRVYTXXXXXXXX 364

+ + I EK N +IND+I \* + + Y\* F + E

Score = 42.0 bits (97), Expect = 0.029

```
Sbjct: 1625 DNQQEKINEKINESENVNENVNINDNINEHEQTYIPFDDDQNEEYDYI----- 1676
Query: 365 XXXXXAPISDSDEFYNTIQIKEYDEQPTYSC-QLLFKKDEE-STDE 408
                    S+ FY+T + + +
                                     SC Q
                                            KKD+
Sbjct: 1677 -----SEFFYSTSEENDMNPNNNLSCKQHELKKDKNYITDE 1712
                                                                      2746
tr Q7RB20
               Hypothetical protein [PY06328] [Plasmodium yoelii
   Q7RB20 PLAYO yoelii]
                                                                      AΑ
                                                                      align
Score = 42.0 bits (97), Expect = 0.029
Identities = 63/306 (20%), Positives = 123/306 (39%), Gaps = 41/306 (13%)
Query: 19 NDTILIEMFN--KYNSEXXXXXXXXXXXYKDNNLIDLSG-YGAKVEV---YDGVELNDKNQ 72
          NDT + E+ N YN+ + D+ +++ Y + +
                                                         D + +N+ +
Sbjct: 39 NDTYVNELNNTSNYNNNNNSNNNMCDKSSDDLNLNIDPCYTNSININSNMDNINMNEDSN 98
Query: 73 FKLTSSANSKIRVTQNQNIIFNSVFL---DFSVSFWIRIPKYKN---DGIQNYIHNEYTI 126
              + N+ + T N N+ ++ DF T.+ Y+N G N +Y+
Sbjct: 99 ----ENMNTYVNTTMNHNVNSSTDSHRNDDFKFHMKINLSAYRNIYEKGKGNAQPKKYNL 154
Query: 127 INCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLN 186
           + K + G ++ DIN + K
                                             RED +N +F+ ++ N+
Sbjct: 155 -SVQKGSKGILLNTYNYYFYNNFGDINKRNKK-----REDD---VNIYFYKKVSRNVP 203
Query: 187 NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMK-YFSIFNTELSQSNI 245
                  ***TD ++ + + + +
                                            QF * Y +F EL +NI
            Y N
Sbjct: 204 NC--YENESNQNDTDDDNVEKSNLDNSKNYNYN-----KQFFGINSYDKVFLKELKITNI 256
Query: 246 EERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYI----KLKKDSPVGEILTRSKY 301
          + +YK +S +Y F P Y+ ++ + +YI
                                                  +K +SP+
Sbjct: 257 DNKYKKKSVKKYNIPF--EPNFYSNRFFFSDKNINENYIGNSKNVKVNSPLSVNNNIESY 314
Query: 302 NQNSKY 307
          N \rightarrow V
Sbjct: 315 NDSEHY 320
tr Q8T186
                                                                       793
               Hypothetical protein [Dictyostelium discoideum (Slime
   Q8T186_DICDI mold)]
                                                                       AΑ
                                                                       align
Score = 41.6 \text{ bits } (96), \text{ Expect = } 0.037
Identities = 50/183 (27%), Positives = 83/183 (45%), Gaps = 37/183 (20%)
Query: 55 YGAKVEVYDGVELNDKNQFKLTSSA----NSKIRVTQ----NQNIIFNSVFLDFSVSFWI 106
          YG + VYD +++N + F + + A N+ I V N N IFN F + ++S
Sbjct: 85 YG-QYSVYDSMDIN-RGSFIMENGAILNVNNSIYVKYYFEINSNSIFNPTFKNTTIS--- 139
Query: 107 RIPKYKNDGIQNYIHNEYTIINCMK---NNSGWKISIRGNRIIWTLIDING----KTKSV 159
                            +NC K NN+G I++ N + I++NG
Sbjct: 140 -TKNFIIGGFLNIYQKSNLFLNCNKLEINNNG-SINVENN----SKINLNGGLIMKDKSQ 193
Query: 160 FFEYNIREDISE---YINRWFFVTITNNLNNAKIYINGKLESNTD----IKDIREVIANG 212
```

```
Sbjct: 1625 DNQQEKINEKINESENVNENVNINDNINEHEQTYIPFDDDQNEEYDYI---- 1676
Query: 365 XXXXXAPISDSDEFYNTIQIKEYDEQPTYSC-QLLFKKDEE-STDE 408
                    S+ FY+T + + +
                                      SC O
                                            KKD+
Sbjct: 1677 -----SEFFYSTSEENDMNPNNNLSCKQHELKKDKNYITDE 1712
                                                                      2746
                Hypothetical protein [PY06328] [Plasmodium yoelii
   Q7RB20 PLAYO yoelii]
                                                                      AA
                                                                      align
 Score = 42.0 \text{ bits } (97), \text{ Expect} = 0.029
 Identities = 63/306 (20%), Positives = 123/306 (39%), Gaps = 41/306 (13%)
Query: 19 NDTILIEMFN--KYNSEXXXXXXXXXXXXYKDNNLIDLSG-YGAKVEV---YDGVELNDKNQ 72
          NDT + E+ N YN+ + D+ +++ Y + + D + +N+ +
Sbjct: 39 NDTYVNELNNTSNYNNNNNSNNNMCDKSSDDLNLNIDPCYTNSININSNMDNINMNEDSN 98
Query: 73 FKLTSSANSKIRVTQNQNIIFNSVFL---DFSVSFWIRIPKYKN---DGIQNYIHNEYTI 126
              + N+ + T N N+ ++ DF T + Y+N G N
Sbjct: 99 ---ENMNTYVNTTMNHNVNSSTDSHRNDDFKFHMKINLSAYRNIYEKGKGNAQPKKYNL 154
Query: 127 INCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLN 186
          + K + G ++ DIN + K RED +N +F+ ++ N+
Sbjct: 155 -SVQKGSKGILLNTYNYYFYNNFGDINKRNKK-----REDD---VNIYFYKKVSRNVP 203
Query: 187 NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMK-YFSIFNTELSQSNI 245
          N Y N +++TD ++ + + + +
                                            QF * Y +F EL +NI
Sbjct: 204 NC--YENESNQNDTDDDNVEKSNLDNSKNYNYN-----KQFFGINSYDKVFLKELKITNI 256
Query: 246 EERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYI----KLKKDSPVGEILTRSKY 301
          + +YK +S +Y F P Y+ ++ + +YI
                                                   4K 48P+
Sbjct: 257 DNKYKKKSVKKYNIPF--EPNFYSNRFFFSDKNINENYIGNSKNVKVNSPLSVNNNIESY 314
Query: 302 NQNSKY 307
          N + Y
Sbjct: 315 NDSEHY 320
                                                                       793
tr Q8T186
                Hypothetical protein [Dictyostelium discoideum (Slime
   Q8T186 DICDI mold)]
                                                                       AA
                                                                       align
 Score = 41.6 bits (96), Expect = 0.037
 Identities = 50/183 (27%), Positives = 83/183 (45%), Gaps = 37/183 (20%)
Query: 55 YGAKVEVYDGVELNDKNQFKLTSSA----NSKIRVTQ----NQNIIFNSVFLDFSVSFWI 106
          YG + VYD +++N + F + + A N+ I V N N IFN F + ++S
Sbjct: 85 YG-QYSVYDSMDIN-RGSFIMENGAILNVNNSIYVKYYFEINSNSIFNPTFKNTTIS--- 139
Query: 107 RIPKYKNDGIQNYIHNEYTIINCMK---NNSGWKISIRGNRIIWTLIDING----KTKSV 159
                G N
                             +NC \times NN+G \quad I++ \quad N \quad + I++NG
Sbjct: 140 -TKNFIIGGFLNIYQKSNLFLNCNKLEINNNG-SINVENN----SKINLNGGLIMKDKSQ 193
Query: 160 FFEYNIREDISE---YINRWFFVTITNNLNNAKIYINGKLESNTD----IKDIREVIANG 212
```

```
+ N +I+ +N+ F N +NN ++I+G L N D + D E+ NG
Sbjct: 194 IYLNNSNIEINGDAMLMNQSIF----NTMNNLDLFISGSLHLNDDSLFLLFDNNEMTING 249
Query: 213 EII 215
         +++
Sbjct: 250 DLL 252
tr Q7RTC2
               Hypothetical protein (Fragment) [PY00072] [Plasmodium
                                                                   3663
   Q7RTC2 PLAYO yoelii
                                                                   AΑ
               yoelii]
                                                                   align
Score = 41.6 bits (96), Expect = 0.037
 Identities = 66/310 (21%), Positives = 125/310 (40%), Gaps = 77/310 (24%)
Query: 45 KDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
         KDN ++ + ++ EV +GV++ N+E,
                                               N +I N+ F+
Sbjct: 6 KDNEVVICNEVVSESEVVNGVKVVSNNEF----- 47
Query: 105 WIRIPKYKNDGIQN-YIHNEYTIINCMKNNSGWKISIR---GNRII---WTL---IDIN 153
               YN * NYN* N *NG+ S GN *+ W * +D N
Sbjct: 48 -----YNNGVVGNFYSENKVVRDNGFVSNIGFGNSNGFNIGNDVVSGSWCVGDNEVDNN 101
Query: 154 GKTKSV-FFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANG 212
          K + F YN +E +N FV NN IY
                                                    D++D
Sbjct: 102 NKVVNYNGFIYNNEVYNNEIVNNNEFVN-----NNGFIY-----NDVRD--HEVVNN 146
Query: 213 EIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEY 272
         +++F D + F I+N E+ +N+ + E ++D N YN E
Sbjct: 147 DVVFYNDEVVRDNGF-----IYNNEVVNNNV-----VFYNDEIVRD---NGFFYNDEV 191
Query: 273 YMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
               N N + + E+++ S++ N++ +N ++Y GE
Sbjct: 192 -----NNNEVVNNNEVVSDNEVVSDSEFIYNNEVVNNNEVYNGEVV----NNNEAVQN 240
Query: 333 DIVRKEDYIY 342
          +++ + + 1
Sbjct: 241 GVIKNYGLMY 250
Score = 36.2 \text{ bits } (82), \text{ Expect} = 1.6
Identities = 44/198 (22%), Positives = 73/198 (36%), Gaps = 38/198 (19%)
Query: 179 VTITNNLNNAKIYING-KLESNTDIKDIREVIANGEIIF------KLDGDI 222
         V I N + + + +NG K+ SN + D EVI N E I+
Sbjct: 10 VVICNEVVSESEVVNGVKVVSNNEFIDNNEVINNNEFIYNNGVVGNFYSENKVVRDNGFV 69
Query: 223 DRTQFIWMKYFSIFNTELSQS-----NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN 276
                  F+I N +S S ++ K+ +Y
                                              , N TYN E Y
Sbjct: 70 SNIGFGNSNGFNIGNDVVSGSWCVGDNEVDNNNKVVNY-----NGFIYNNEVYNNE 120
Query: 277 AGNKNSYIK----LKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
           N N ++ D E++ N ++
                                                  + + + +N ND
Sbjct: 121 IVNNNEFVNNNGFIYNDVRDHEVVNNDVVFYNDEVVRDNGFIYNNEVV---NNNVVFYND 177
Query: 333 DIVRKEDYIYLDFFNLNQ 350
```

```
+ N +I+ +N+ F N +NN ++I+G L N D + D E+ MG
Sbjct: 194 IYLNNSNIEINGDAMLMNQSIF----NTMNNLDLFISGSLHLNDDSLFLLFDNNEMTING 249
Query: 213 EII 215
          +++
Sbjct: 250 DLL 252
tr Q7RTC2
               Hypothetical protein (Fragment) [PY00072] [Plasmodium
   Q7RTC2_PLAYO yoelii
                                                                    AA
                                                                    aliqn
               yoelii]
 Score = 41.6 bits (96), Expect = 0.037
 Identities = 66/310 (21%), Positives = 125/310 (40%), Gaps = 77/310 (24%)
Query: 45 KDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
          KDN ++ + ++ EV +GV++ N+E
Sbjct: 6 KDNEVVICNEVVSESEVVNGVKVVSNNEF-----IDNNEVINNNEFI----- 47
Query: 105 WIRIPKYKNDGIQN-YIHNEYTIINCMKNNSGWKISIR---GNRII---WTL---IDIN 153
               YN * NY N* N +N G+ S GN ++ W *
Sbjct: 48 ----YNNGVVGNFYSENKVVRDNGFVSNIGFGNSNGFNIGNDVVSGSWCVGDNEVDNN 101
Query: 154 GKTKSV-FFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANG 212
           K + F YN +E +N FV NN IY
                                                     D++D
Sbjct: 102 NKVVNYNGFIYNNEVYNNEIVNNNEFVN-----NNGFIY------NDVRD--HEVVNN 146
Query: 213 EIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEY 272
          +++F D + F I+N E+ +N+ + E ++D N
Sbjct: 147 DVVFYNDEVVRDNGF-----IYNNEVVNNNV----VFYNDEIVRD---NGFFYNDEV 191
Query: 273 YMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
               N N + + E+++ S++ N++ +N ++Y GE
Sbjct: 192 -----NNNEVVNNNEVVSDNEVVSDSEFIYNNEVVNNNEVYNGEVV-----NNNEAVQN 240
Query: 333 DIVRKEDYIY 342
           +++ + +  
Sbjct: 241 GVIKNYGLMY 250
 Score = 36.2 \text{ bits } (82), \text{ Expect = } 1.6
 Identities = 44/198 (22%), Positives = 73/198 (36%), Gaps = 38/198 (19%)
Query: 179 VTITNNLNNAKIYING-KLESNTDIKDIREVIANGEIIF------KLDGDI 222
          V I N + + + +NG K+ SN + D EVI N E I+
                                                            * *C+ +
Sbjct: 10 VVICNEVVSESEVVNGVKVVSNNEFIDNNEVINNNEFIYNNGVVGNFYSENKVVRDNGFV 69
Query: 223 DRTQFIWMKYFSIFNTELSQS-----NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN 276
                  F+I N +S S ++ K+ +Y
                                               N +YN E Y
Sbjct: 70 SNIGFGNSNGFNIGNDVVSGSWCVGDNEVDNNNKVVNY-----NGFIYNNEVYNNE 120
Query: 277 AGNKNSYIK----LKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
           N N ++ + D E++ N + +
                                                    + +
Sbjct: 121 IVNNNEFVNNNGFIYNDVRDHEVVNNDVVFYNDEVVRDNGFIYNNEVV---NNNVVFYND 177
Query: 333 DIVRKEDYIYLDFFNLNQ 350
```

+IVR + Y D N N+ Sbjct: 178 EIVRDNGFFYNDEVNNNE 195

378 tr <u>Q7RFF5</u> Arabinogalactan protein [PY04751] [Plasmodium yoelii Q7RFF5 PLAYO yoelii] AΑ align Score = 40.8 bits (94), Expect = 0.064Identities = 42/176 (23%), Positives = 80/176 (44%), Gaps = 20/176 (11%) Query: 182 TNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRT---QFIWMKYFSIFNT 238 + N NN+ +N K+ DI+ + +I N + K D +++ Q I÷ Sbjct: 104 SENSNNSDNVLNNKI----DIEKDKNIIVNKSDL-KDDDNLNTKKMDQIIYKSIQSNYDK 158 Query: 239 EL-SQSNIEERYKIQSYSEYLKDFW----GNPLMYNKEYY--MFNA----GNKNSYIKLK 287 E +++N++E Y++ Y++ K++ NP K YY + N+ Sbjct: 159 EFFAKNNLQEEYQLH-YNKLSKEYEFFEDDNPYKNKKCYYGNISNSDKIRGNEQYINNSN 217 Query: 288 KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYL 343 +S + + N KY + D+ + + K N+ S ND Sbjct: 218 SESEINSDYDSNDSNFKKKYYEFNDIDFDQIYKYIYKKNNVSENDKFKFKRDHLYL 273

tr Q8ILN7 Hypothetical protein [PF14 0206] [Plasmodium falciparum 910 Q8ILN7\_PLAF7 (isolate AA 3D7)] align Score = 40.4 bits (93), Expect = 0.083Identities = 55/278 (19%), Positives = 106/278 (37%), Gaps = 53/278 (19%)

+ ND

YIH++

+ +++N I +N NII+ +F Sbjct: 347 IDNNSNVMIHFNKNDNIIYKDIFKKLDEERKQKKDNIYNDYAHKYIHSDMLYNYRVVQND 406

Query: 75 LTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNS 134

Query: 135 GWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYING 194 I L ++N +FF N+ +DI\*+ + ++

Sbjct: 407 LYKI-----IQPVLYNLN----IFFNQNVIKDINKIMEKY------ 437

Query: 195 KLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSY 254 +T I+D+++V E +++ +++ Y EH QHNH H

Sbjct: 438 ----DTVIQDVQQVGRKKEYNKRINEGLEKREGHKSTYEK--ENEVKQNNVTQNGD---- 487

Query: 255 SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNONS----- 305 K N Y +EY N N + I KK

Sbjct: 488 ----KKLQNNVQTYEQEYIQTNLHNDDKNINTKKIQNSKNYHVNEKRNDKNVDNKNKDKE 543

Query: 306 KYINYRDLYIGEKFIIRR-KSNSQSINDDIVRKEDYIY 342

+ INY +L G+K I+ K + + + RKE+ ++ Sbjct: 544 ECINYTELDKGDKHIMNTLKIPNNKMQKEEKRKENVLF 581

tr Q8I462 Hypothetical protein PFE0190c [PFE0190c] [Plasmodium 662 +IVR + Y D N N+ Sbjct: 178 EIVRDNGFFYNDEVNNNE 195

tr <u>Q7RFF5</u> Arabinogalactan protein [PY04751] [Plasmodium yoelii 378 Q7RFF5 PLAYO yoelii] AA <u>align</u> Score = 40.8 bits (94), Expect = 0.064Identities = 42/176 (23%), Positives = 80/176 (44%), Gaps = 20/176 (11%) Query: 182 TNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRT---QFIWMKYFSIFNT 238 + N NN+ +N K+ DI+ + +I N + K D +++ Q I+ Sbjct: 104 SENSNNSDNVLNNKI----DIEKDKNIIVNKSDL-KDDDNLNTKKMDQIIYKSIQSNYDK 158 Query: 239 EL-SQSNIEERYKIQSYSEYLKDFW----GNPLMYNKEYY--MFNA----GNKNSYIKLK 287 E +++N++E Y++ Y++ K++ NP K YY + N+ Sbjct: 159 EFFAKNNLQEEYQLH-YNKLSKEYEFFEDDNPYKNKKCYYGNISNSDKIRGNEQYINNSN 217 Query: 288 KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYL 343 +S + + N KY + D+ + + K N+ S ND Sbjct: 218 SESEINSDYDSNDSNFKKKYYEFNDIDFDQIYKYIYKKNNVSENDKFKFKRDHLYL 273 tr <u>Q8ILN7</u> Hypothetical protein [PF14 0206] [Plasmodium falciparum Q8ILN7 PLAF7 (isolate AΑ 3D7)] align Score = 40.4 bits (93), Expect = 0.083Identities = 55/278 (19%), Positives = 106/278 (37%), Gaps = 53/278 (19%) Query: 75 LTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNS 134 + +++N I +N NII+ +F + ND YIH++ Sbjct: 347 IDNNSNVMIHFNKNDNIIYKDIFKKLDEERKQKKDNIYNDYAHKYIHSDMLYNYRVVQND 406 Query: 135 GWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYING 194 +KI I L ++N +FF N+ +DI\*+ + ++ Sbjct: 407 LYKI-----IQPVLYNLN-----IFFNQNVIKDINKIMEKY------ 437 Query: 195 KLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSY 254 +T I+D+++V E +++ +++ + X EH OHNH H Sbjct: 438 ----DTVIQDVQQVGRKKEYNKRINEGLEKREGHKSTYEK--ENEVKQNNVTQNGD---- 487 Query: 255 SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNONS----- 305 K N  $X \rightarrow EX \qquad N \qquad N \rightarrow \qquad I \qquad KK$ Sbjct: 488 ----KKLQNNVQTYEQEYIQTNLHNDDKNINTKKIQNSKNYHVNEKRNDKNVDNKNKDKE 543 Query: 306 KYINYRDLYIGEKFIIRR-KSNSQSINDDIVRKEDYIY 342 + INY +L G+K I+ K + + + RKE+ ++ Sbjct: 544 ECINYTELDKGDKHIMNTLKIPNNKMQKEEKRKENVLF 581

tr Q8I462 Hypothetical protein PFE0190c [PFE0190c] [Plasmodium 662

AΑ

```
Q8I462_PLAF7 falciparum
              (isolate 3D7)]
                                                               align
Score = 40.4 bits (93), Expect = 0.083
Identities = 44/204 (21%), Positives = 78/204 (37%), Gaps = 27/204 (13%)
Query: 98 LDFSVSFWIRIPKYKNDGIQNYIHNEYT-----IINCMKNNSGWKISIRGNRIIW 147
         +D+ + + + I + K D + N + E
                                        I X N +++ I++ +R
Sbjct: 94 VDYHLQYVSNIFEKKKDELNNIMEKEKKSMSIDELICDIINYLESVINGNINVDNHRFNH 153
Query: 148 TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNL-NNAKIYINGKLESNTDIKDIR 206
           I+I K + NI +I+ IN I NN+ NN IN
Query: 207 EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPL 266
         \pm G \pm L\pm \pm YF F E \pm N\pm \pm \pm
Sbjct: 214 KCSGGGSFLKNLN-----LSYFKDFLVERKKINLDALFNDNSLNVLFDELY---- 259
Query: 267 MYNKEYYMFNAGNKN--SYIKLKK 288
         Y Y + N N +TK+K+
Sbjct: 260 TYTYIYLLINYKRNNFFDFIKMKR 283
```

```
tr Q7RRG0 Protein kinase domain, putative [PY00761] [Plasmodium
                                                               2941
   Q7RRG0_PLAYO yoelii yoelii]
                                                               AΑ
                                                               align
Score = 40.4 bits (93), Expect = 0.083
Identities = 85/409 (20%), Positives = 151/409 (36%), Gaps = 105/409 (25%)
          GVELNDKNQFKLTSSANSKIRVTQNQNIIFN----SVFLDFSVSFWIRIPKYKNDGIQNY 119
          G+ +N + AN K+ NI+ N ++ L + ++ I
Sbjct: 1720 GINMNTNGTVNRNTVANYKVN----NILINDKLKNILLSKNFDHFL-IENENKIGIRNS 1773
Query: 120 IHNEYTIINCMK--NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNI-----RED 168
          I+N Y+ + NN+G + GN NG V + NI +E
Sbjct: 1774 INNSYSNTGNVNHNNNAGRTVGANGNCTSNENCTPNGTNIGVLKDSNILSGNMIPKLKES 1833
Query: 169 ISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFI 228
          + Y + + NN+ N EI N ++ NT+ I+
Sbjct: 1834 YNYYSHFKSQIPSNNNVINKKITENTEISENTENNKIQ------GINR---- 1875
Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKE-YYMFNAGNKNSYIKLK 287
               I+N + Q N +E + EY + NK ++ NA N +YI+
Sbjct: 1876 -----IYNNYIGQGNTKENIPMNVNKEYSNKHISD---INKSIFFSQNANNSLNYIE-- 1924
Query: 288 KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRR--KSNSQSINDDIVRKEDYIYLDF 345
                       S Y Y + K IRR K+ ++ND+++
Sbjct: 1925 ----- 1960
Query: 346 FNLNQEWRVYTXXXXXXXXXXXXPISDSDEFYNTIQIKEYDEQP----TYSCQLLFKK 401
            NQ+ ++Y
                         I + +++XN I I+E + + P++K+
Sbjct: 1961 ---NQQRQIY------QIENENKYYNNINIQEGINKKIANLNFQDILIYKQ 2002
Query: 402 DEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
          Sbjct: 2003 NNLNIDQIN----KKKYDSN--FNNYLNSTAITSISNKNIPRQFTNAKI 2045
```

AA Q8I462\_PLAF7 falciparum align (isolate 3D7)] Score = 40.4 bits (93), Expect = 0.083Identities = 44/204 (21%), Positives = 78/204 (37%), Gaps = 27/204 (13%) Query: 98 LDFSVSFWIRIPKYKNDGIQNYIHNEYT-----IINCMKNNSGWKISIRGNRIIW 147 +D+ + + I + K D + N + E IIN +++ I++ +R Sbjct: 94 VDYHLQYVSNIFEKKKDELNNIMEKEKKSMSIDELICDIINYLESVINGNINVDNHRFNH 153 Query: 148 TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNL-NNAKIYINGKLESNTDIKDIR 206 I+I K + NI +I+ IN I NN+ NN IN Query: 207 EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPL 266  $+ \quad G \quad + \quad L + \qquad \qquad + \quad YF \quad F \quad E \quad + \quad N + + \quad \quad S \quad + \qquad + \quad + \quad \quad$ Sbjct: 214 KCSGGGSFLKNLN------LSYFKDFLVERKKINLDALFNDNSLNVLFDELY---- 259 Query: 267 MYNKEYYMFNAGNKN--SYIKLKK 288 Y Y + N N +IK+K+ Sbjct: 260 TYTYIYLLINYKRNNFFDFIKMKR 283

tr Q7RRG0 Protein kinase domain, putative [PY00761] [Plasmodium 2941 Q7RRG0\_PLAYO **yoelii yoelii**] <u>align</u> Score = 40.4 bits (93), Expect = 0.083Identities = 85/409 (20%), Positives = 151/409 (36%), Gaps = 105/409 (25%) Query: 64 GVELNDKNQFKLTSSANSKIRVTQNQNIIFN----SVFLDFSVSFWIRIPKYKNDGIQNY 119 G+ +N + AN K+ NI+ N ++ L + ++ I GI+N Sbjct: 1720 GINMNTNGTVNRNTVANYKVN-----NILINDKLKNILLSKNFDHFL-IENENKIGIRNS 1773 Query: 120 IHNEYTIINCMK--NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNI-----RED 168 I+N Y+ + NN+G + GN NG V + NI +E Sbjct: 1774 INNSYSNTGNVNHNNNAGRTVGANGNCTSNENCTPNGTNIGVLKDSNILSGNMIPKLKES 1833 Query: 169 ISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFI 228 + Y + + MN+ N KT N ++ NT+ I+ Sbjct: 1834 YNYYSHFKSQIPSNNNVINKKITENTEISENTENNKIQ------GINR---- 1875 Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKE-YYMFNAGNKNSYIKLK 287 I+N + Q N +E + EY + NX ++ NA N +YI+ Sbjct: 1876 -----IYNNYIGQGNTKENIPMNVNKEYSNKHISD---INKSIFFSQNANNSLNYIE-- 1924 Query: 288 KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRR--KSNSQSINDDIVRKEDYIYLDF 345 SYY + K IRR K+ ++ND+++ Sbjct: 1925 ----- 1960 Query: 346 FNLNQEWRVYTXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP----TYSCQLLFKK 401 I + +++YN I I+E + + L++K+ NQ+ ++Y Sbjct: 1961 ---NQQRQIY------QIENENKYYNNINIQEGINKKIANLNFQDILIYKQ 2002 Query: 402 DEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450 Sbjct: 2003 NNLNIDQIN----KKKYDSN--FNNYLNSTAITSISNKNIPRQFTNAKI 2045

```
tr <u>Q7RPW6</u>
              Hypothetical protein (Fragment) [PY01338] [Plasmodium
                                                                    3644
   Q7RPW6 PLAYO yoelii yoelii]
                                                                    AΑ
                                                                    align
 Score = 40.4 bits (93), Expect = 0.083
 Identities = 69/315 (21%), Positives = 134/315 (41%), Gaps = 33/315 (10%)
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXRYKDNNLIDLSGYG-AKVEV 61
           Sbjct: 3012 NKYISKIN----IKHSNDILMYEKEHTGSLDNISHQSTDDRKNNDNIENENHYNNSKLE- 3066
          YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH 121
              ++N K +++ +R +N+ +F ++ + I I K+ N+ +++
Sbjct: 3067 --NSQINPKEDNNTLNNSIYMLRKQKNEKKLFELYYIYIYII--IHIIKFYNE---SFVD 3119
Query: 122 NEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE--DISEYINRWFFV 179
           +Y I MC+ I + I + N K+ S + +N E DI+E+I+
Sbjct: 3120 LKYYIYNCI-----CEIASSYIPFYFTQNNIKSFSYYSNHNSEENKDINEFISFINNI 3172
Query: 180 TITNNLNNAKIY--INGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFN 237
           I+ N+N+ K+Y N K E K I + N +
Sbjct: 3173 NISTNVNDLKLYNFNNKKKEKKLKSKKILKKTYNSDNENDHHTQASKLEFIQSPKSA--- 3229
Query: 238 TELSQSNIEERYKIQSYSEYL--KDFWGNPLMYNKEYYMFNAGNK----NSYIKLKKDSP 291
          T++N SS+++FN +Y+N+N+
Sbjct: 3230 TKTYEENEYSEIPGSSISTFIGTEKFSSNESGIERIYNLSNSKNERIENNSCIEQKKNSR 3289
Query: 292 VGEILTRSKYNQNSK 306
             I T+ K QN +
Sbjct: 3290 SICIDTKLKNIQNPR 3304
Score = 40.0 \text{ bits (92)}, Expect = 0.11
Identities = 69/332 (20%), Positives = 124/332 (36%), Gaps = 71/332 (21%)
Query: 55 YGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKND 114
         Y \rightarrow + + + + + N+ + + T+ N N \rightarrow N+F+ + + + + YKN+
Sbjct: 353 YNDQYVISNYIKQNNNEIEVITTDGNRNNTSLVNLQKLKNNNFIKNNHTIYTKPIIYKNN 412
Query: 115 GIQN-----YIHNEYTIINCM-----KNNSGWKI---SIRGNRIIWTL 149
               XI N+ +N
                                            K+ G I S G+RII
Sbjct: 413 KLYNSYNYINQNLEYIQNDVNNMNTSNIHKIVRENIPPKSQDGPFINETSNLGSRII--- 469
Query: 150 IDINGKTKSVFFEYNIREDISEYINRWFFVTI-------TUNLNNAKIY 191
            NG + ++ N+ + + IN +
Sbjct: 470 ---NGNASTSLYDKNVENNNANNINSALNTNVDLKFHSKTGISNLHVKNCTNNINKLMIS 526
Query: 192 INGKLESNTDIKDIREVIANGEIIFKLDGDIDRT---QFIWMKYFSIFNTELSQSNI-EE 247
            K E+ ++K++++ +I G+I T W
                                                  4-4- N
Sbjct: 527 YRNKEEAKENVKNVKKETYINDINSSNGGNIINTIASNMKWNNNSNMINNIASMNNINKE 586
Query: 248 RYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKY 307
          *+ I+ K + N +YN * M + N N LK + P K N N
Sbjct: 587 KHWIK-----KTYLDNTDIYNAD-KMSVSSNMNKLYDLKNEKP-----KKNNNDLN 631
```

```
tr Q7RPW6
              Hypothetical protein (Fragment) [PY01338] [Plasmodium
                                                                  3644
   Q7RPW6 PLAYO yoelii yoelii]
                                                                   <u>align</u>
 Score = 40.4 bits (93), Expect = 0.083
 Identities = 69/315 (21%), Positives = 134/315 (41%), Gaps = 33/315 (10%)
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYG-AKVEV 61
          NKY+ I ++ND ++ E + + + + R ++N+ + + Y +K+E
Sbjct: 3012 NKYISKIN----IKHSNDILMYEKEHTGSLDNISHQSTDDRKNNDNIENENHYNNSKLE- 3066
          YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH 121
              ++N K +++ +R +N+ +F ++ + I I K+ N+ +++
Sbjct: 3067 -- NSQINPKEDNNTLNNSIYMLRKQKNEKKLFELYYIYIYII--IHIIKFYNE---SFVD 3119
Query: 122 NEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE--DISEYINRWFFV 179
           Sbjct: 3120 LKYYIYNCI----CEIASSYIPFYFTQNNIKSFSYYSNHNSEENKDINEFISFINNI 3172
Query: 180 TITNNLNNAKIY--INGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFN 237
           I+ N+N+ K+Y N K E K I + N +
Sbjct: 3173 NISTNVNDLKLYNFNNKKKEKKLKSKKILKKTYNSDNENDHHTQASKLEFIQSPKSA--- 3229
Query: 238 TELSQSNIEERYKIQSYSEYL--KDFWGNPLMYNKEYYMFNAGNK----NSYIKLKKDSP 291
          T+ + N SS+++FN +Y+N+N+ NSI+KK+S
Sbjct: 3230 TKTYEENEYSEIPGSSISTFIGTEKFSSNESGIERIYNLSNSKNERIENNSCIEQKKNSR 3289
Query: 292 VGEILTRSKYNQNSK 306
             I T+ K QN +
Sbjct: 3290 SICIDTKLKNIQNPR 3304
Score = 40.0 \text{ bits } (92), \text{ Expect} = 0.11
Identities = 69/332 (20%), Positives = 124/332 (36%), Gaps = 71/332 (21%)
Query: 55 YGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKND 114
         Y + + + + + N+ +T+ N N + N+ F+ + + + + XKN+
Sbjct: 353 YNDQYVISNYIKQNNNEIEVITTDGNRNNTSLVNLQKLKNNNFIKNNHTIYTKPIIYKNN 412
Query: 115 GIQN-----YIHNEYTIINCM-----KNNSGWKI---SIRGNRIIWTL 149
          + N Y X N+ +N
                                           K+ G I S G+RII
Sbjct: 413 KLYNSYNYINQNLEYIQNDVNNMNTSNIHKIVRENIPPKSQDGPFINETSNLGSRII--- 469
Query: 150 IDINGKTKSVFFEYNIREDISEYINRWFFVTI-----TUNLNNAKIY 191
           NG + ++ N+ + IN +
Sbjct: 470 ---NGNASTSLYDKNVENNNANNINSALNTNVDLKFHSKTGISNLHVKNCTNNINKLMIS 526
Query: 192 INGKLESNTDIKDIREVIANGEIIFKLDGDIDRT---QFIWMKYFSIFNTELSQSNI-EE 247
            K E+ ++K++++ +I G+I T W ++ N
                                                         S +NT +E
Sbjct: 527 YRNKEEAKENVKNVKKETYINDINSSNGGNIINTIASNMKWNNNSNMINNIASMNNINKE 586
Query: 248 RYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKY 307
          ++ I+ K + N +YN + M + N N LK + P K N N
Sbjct: 587 KHWIK-----KTYLDNTDIYNAD-KMSVSSNMNKLYDLKNEKP-----KKNNNDLN 631
```

```
Query: 308 INYRDLYIGEKFIIRRKSNSQSINDDIVRKED 339
         IN D+ I + + NS N+ + K D
Sbjct: 632 INNTDMVINSR---KCSENSTENNNRQIMKND 660
Score = 36.2 \text{ bits } (82), \text{ Expect = } 1.6
 Identities = 42/168 (25%), Positives = 72/168 (42%), Gaps = 16/168 (9%)
Query: 19 NDTILIEMFNKYNSEXXXXXXXXXXXKYKDNNLIDLSGYGAKVEVYDGV-ELNDKNQFKLTS 77
         Sbjct: 823 NDTTNINLSNQYINKNFMPTHIIN--DDENLLG----STKMSSFDGITKLEDEKNIEYLT 876
Query: 78 SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWK 137
             I +N ++N+ ++ KXK D + I+NE +N
Sbjct: 877 GEYYYINGKMEENKLYNNENINC-----FRKYK-DMLNTNINNEKYNVNGKYNRNNLS 928
Query: 138 ISIRGNRIIWTL-IDINGKTKSVFFEYNIREDISEYINRWFFVTITNN 184
          S+ N T I NGK KS +YN++ ++ +N F+ I NN
Sbjct: 929 PSVNINDKANTKNITENGKYKSYQKDYNLKTFKNKSVNPQSFLQIKNN 976
           Mitochondrial ribosomal protein VAR1 [VAR1] [Candida
                                                                    339
sp <u>P21358</u>
```

```
RMAR CANGA glabrata
                                                                    AΑ
             (Yeast) (Torulopsis glabrata)]
                                                                     <u>align</u>
Score = 40.0 \text{ bits } (92), \text{ Expect} = 0.11
Identities = 71/314 (22%), Positives = 118/314 (36%), Gaps = 58/314 (18%)
Query: 28 NKYNSEXXXXXXXXXXYKDNNLIDLSGYGAK----VEVYDGVELNDKNQFKLTSSANSKI 83
         NEY SE + N L Y + Y +L +K +EL S N+KI
Sbjct: 41 NKYLSELNNKGNSLQHLNNMNNWKLQNYNYNKNNTINNYINSKLINKLLYKLMSLKNNKI 100
Query: 84 RVTQ-----NQNII------FNSVFLDFSVSFWIRIPKYKN------DGIQNYIH 121
          +++ N N+I
                             N+ ++++ I K N
Sbjct: 101 IISKPLYKINMNVINIRFYYYNMNNYNYNNNIYYINMINKLMNRLNINMNNLSNILSYYY 160
Query: 122 NEYTIINCMKNNSGWKISIRGNRIIW---TLIDINGKTKSVFFEY----NIREDISEYI 173
         N+ II +K
                    K NI+ +L+DN + EY
Sbjct: 161 NKKVIIEPIK----LKYLYNNNEIMTKYISLLDNNKYNNGLLMEYQRTLNNIMPKLNDHN 216
Query: 174 NRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF 233
                 NN+N K Y N L +N +I +I I
                                                 ++ **+ 2 ** +
Sbjct: 217 ISMNYINNINNINKLK-YNNILLNNNNNINNIYNNI-----NINNNMNLLMFKYLIGW 268
Query: 234 SIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG 293
             NI S + N NK+Y GN N+ KL +
Sbjct: 269 SIMLKGRLNKNI------SRISTTYLNNGTFNNKKYLW---GNLNNNFKLNYINSNN 316
Query: 294 EILTRSKYNQNSKY 307
          T + M+M KX
Sbjct: 317 NIYNYNNINKNGKY 330
```

tr Q8II48 Hypothetical protein [PF11\_0326] [Plasmodium falciparum 2763

Query: 308 INYRDLYIGEKFIIRRKSNSQSINDDIVRKED 339 IN D+ I + + NS N+ + K D Sbjct: 632 INNTDMVINSR---KCSENSTENNNRQIMKND 660 Score = 36.2 bits (82), Expect = 1.6Identities = 42/168 (25%), Positives = 72/168 (42%), Gaps = 16/168 (9%) Query: 19 NDTILIEMFNKYNSEXXXXXXXXXXXXYKDNNLIDLSGYGAKVEVYDGV-ELNDKNOFKLTS 77 NDT T + N+Y ++ D NL+ K+ +DG+ +L D+ + + Sbjct: 823 NDTTNINLSNQYINKNFMPTHIIN--DDENLLG----STKMSSFDGITKLEDEKNIEYLT 876 Query: 78 SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWK 137 +M ++M+ ++ KXK D + I+ME +N Sbjct: 877 GEYYYINGKMEENKLYNNENINC-----FRKYK-DMLNTNINNEKYNVNGKYNRNNLS 928 Query: 138 ISIRGNRIIWTL-IDINGKTKSVFFEYNIREDISEYINRWFFVTITNN 184 S+ N T I NGK KS +YN++ ++ +N F+ I NN Sbjct: 929 PSVNINDKANTKNITENGKYKSYQKDYNLKTFKNKSVNPQSFLQIKNN 976 sp P21358 339 Mitochondrial ribosomal protein VAR1 [VAR1] [Candida RMAR CANGA glabrata AΑ

(Yeast) (Torulopsis glabrata)] align Score = 40.0 bits (92), Expect = 0.11Identities = 71/314 (22%), Positives = 118/314 (36%), Gaps = 58/314 (18%) Query: 28 NKYNSEXXXXXXXXXXXXXKYKDNNLIDLSGYGAK----VEVYDGVELNDKNQFKLTSSANSKI 83 NEY SE + N L Y + Y +L +K +KL S N+KI Sbjct: 41 NKYLSELNNKGNSLQHLNNMNNWKLQNYNYNKNNTINNYINSKLINKLLYKLMSLKNNKI 100 Query: 84 RVTQ----NQNII-----FNSVFLDFSVSFWIRIPKYKN-----DGIQNYIH 121 +++ N: N+I N+ ++++ I K N Sbjct: 101 IISKPLYKINMNVINIRFYYYNMNNYNYNNNIYYINMINKLMNRLNINMNNLSNILSYYY 160 Query: 122 NEYTIINCMKNNSGWKISIRGNRIIW---TLIDINGKTKSVFFEY----NIREDISEYI 173 N+ II +K K N I+ +L+D N + EY NI Sbjct: 161 NKKVIIEPIK----LKYLYNNNEIMTKYISLLDNNKYNNGLLMEYQRTLNNIMPKLNDHN 216 Query: 174 NRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF 233 NN+N K Y N L +N +I +I I 4--4- $+++ **+ \overline{E} **+ +$ Sbjct: 217 ISMNYINNINNINKLK-YNNILLNNNNNINNIYNNI-----NINNNMNLLMFKYLIGW 268 Query: 234 SIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG 293 NI S + M NK+Y GN M+ KL + Sbjct: 269 SIMLKGRLNKNI------SRISTTYLNNGTFNNKKYLW---GNLNNNFKLNYINSNN 316 Query: 294 EILTRSKYNQNSKY 307 I + N+N KX

Sbjct: 317 NIYNYNNINKNGKY 330

Hypothetical protein [PF11\_0326] [Plasmodium falciparum 2763

Q8II48 PLAF7 (isolate

AΑ

3D7)] align Score = 40.0 bits (92), Expect = 0.11Identities = 67/278 (24%), Positives = 119/278 (42%), Gaps = 33/278 (11%) Query: 46 DNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFW 105 D+N D+Y Y+ N+KN YK + +K + +N+ I+ SVY + +Sbjct: 537 DSNDDDNNNYYYYSNNYNNNYRNKNNFKRNNFEINKEK--ENKEKIYTSVFEENNK--- 591 Query: 106 IRIPKYKNDGIQNYIH-NEYTIINCMKNNSGWKISIRGNRIIWTLIDIN-GKTKSVFFEY 163 N+I+ NE K+N I + + IDI+ K ++FF++ Sbjct: 592 VIIDMINNKNKDNFININE-----KSNEITNIHNYTDVYVDEDIDIHVDKNNNIFFDH 644 Query: 164 NIREDISEYINRWFFVTITNNLNNAKIYINGKL----ESNTDIKDIREVIANGEIIFKL 218 + ++ N + N +N + Y N KL E+N K+, + I E ++ N Sbjct: 645 NSNFFVDDFNNLHVY----NKHNEEYYKNIKLYNRFMENNKTGKENYDYIQEYEYEYEY 699 Query: 219 DGDIDRTQFIWMKYFSIFNTELSQSNIEER-YKIQSYSEYLKDFWGNPLMYNKEYYMFNA 277 + D D + M Y I+N ++ ++N + + I +Y + P M N + N Sbjct: 700 E-DEDLSNNYNMDY--IYNDQIQRNNDSQIIHDINNYDIF--SILSIPNMNNNDN---NN 751 Query: 278 GNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYI 315 N N ++ S ++N+ Y MY+D YI Sbjct: 752 DNNNDNNNNNNNNNNNNNYYYSSSSSKNNNYYNYQDRYI 789 tr Q8I2R1 Hypothetical protein PFI1210w [PFI1210w] [Plasmodium 2082 Q8I2R1\_PLAF7 falciparum AA<u>align</u> (isolate 3D7)] Score = 40.0 bits (92), Expect = 0.11Identities = 55/287 (19%), Positives = 106/287 (36%), Gaps = 35/287 (12%) Query: 65 VELNDKNQFKLTSSANSKIRVT-----QNQNIIFNSVFLDF-SVSFWIRIP 109 + +ND + L SS KI + + +N + ++ ++ ++S ++ Sbjct: 10 MNINDYEEKNLNSSGEKKINIKIGDLASHNSGNFDEEKKNSVCKNLIVNMPNISKGVQEE 69 Query: 110 KYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI 169 + K + + + NE +IN +K+ + G K E + Sbjct: 70 ECKIEELDKVVRNEMDMINSLKDEK------VIGMDKMYDMEKEKDMCL 112 Query: 170 SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIW 229 N + F N I+ + +N I + E N + + ID T+ Sbjct: 113 INEKNSYSFGKDKKKNNIDGIHNIHHISANDHIINPNEYKPNVQNLVSNSTHIDSTEICS 172 Query: 230 MKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK- 288 + ++ I Y E+ K + + N+ Y N N MS + L + Sbjct: 173 SKFVKEEEHNNDNNEYDKNVHILKYPEHNKTKDMDNNLSNQYLYSCNISNNNSQLHLSRL 232 Query: 289 -DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDI 334 E L K N KY N ++ + + + TR SN+ + N++1 Sbjct: 233 FDKETDE-LNSIKVNNQDKYDNMSEIKLEKTLMIRDNSNNNNNNNNI 278

AA Q8II48 PLAF7 (isolate align -3D7)] Score = 40.0 bits (92), Expect = 0.11Identities = 67/278 (24%), Positives = 119/278 (42%), Gaps = 33/278 (11%) Query: 46 DNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFW 105 Sbjct: 537 DSNDDDNNNYYYYSNNYNNNYRNNKNNFKRNNFEINKEK--ENKEKIYTSVFEENNK--- 591 Query: 106 IRIPKYKNDGIQNYIH-NEYTIINCMKNNSGWKISIRGNRIIWTLIDIN-GKTKSVFFEY 163 + I N N+I+ NE K+N I + + IDI+ K ++FF++ Sbjct: 592 VIIDMINNKNKDNFININE-----KSNEITNIHNYTDVYVDEDIDIHVDKNNNIFFDH 644 Query: 164 NIREDISEYINRWFFVTITNNLNNAKIYINGKL----ESNTDIKDIREVIANGEIIFKL 218 N + ++ N + N +N + Y N KL E+N K+ + I E ++ . Sbjct: 645 NSNFFVDDFNNLHVY----NKHNEEYYKNIKLYNRFMENNKTGKENYDYIQEYEYEYEY 699 Ouery: 219 DGDIDRTOFIWMKYFSIFNTELSOSNIEER-YKIOSYSEYLKDFWGNPLMYNKEYYMFNA 277 + D D + M Y I+N ++ ++N + + I +Y + P M N + N Sbjct: 700 E-DEDLSNNYNMDY--IYNDQIQRNNDSQIIHDINNYDIF--SILSIPNMNNNDN---NN 751 Query: 278 GNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYI 315 N N ++ S ++N+ Y NY+D YI Sbjct: 752 DNNNDNNNNNNNNNNNNNYYYSSSSSKNNNYYNYQDRYI 789 tr Q8I2R1 Hypothetical protein PFI1210w [PFI1210w] [Plasmodium 2082 Q8I2R1 PLAF7 falciparum AΑ <u>align</u> (isolate 3D7)] Score = 40.0 bits (92), Expect = 0.11Identities = 55/287 (19%), Positives = 106/287 (36%), Gaps = 35/287 (12%) Query: 65 VELNDKNQFKLTSSANSKIRVT-----QNQNIIFNSVFLDF-SVSFWIRIP 109 + +ND + L SS KI + \* +N + \*+ ++ \*\*S ++ Sbjct: 10 MNINDYEEKNLNSSGEKKINIKIGDLASHNSGNFDEEKKNSVCKNLIVNMPNISKGVQEE 69 Query: 110 KYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI 169 + K + + + NE +IN +K+ +GKE+ Sbjct: 70 ECKIEELDKVVRNEMDMINSLKDEK------VIGMDKMYDMEKEKDMCL 112 Query: 170 SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIW 229 N + F N I+ + +N I + E N + + ID T+ Sbjct: 113 INEKNSYSFGKDKKKNNIDGIHNIHHISANDHIINPNEYKPNVQNLVSNSTHIDSTEICS 172 Query: 230 MKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK- 288 + ++ I Y E+ K + + N+ Y N N MS + L + Sbjct: 173 SKFVKEEEHNNDNNEYDKNVHILKYPEHNKTKDMDNNLSNQYLYSCNISNNNSQLHLSRL 232 Query: 289 -DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDI 334 E L K N KY N ++ + + + TR SN+ + N++1 Sbjct: 233 FDKETDE-LNSIKVNNQDKYDNMSEIKLEKTLMIRDNSNNNNNNNNN 278

```
3195
tr Q7RQ77
                Hypothetical protein [PY01225] [Plasmodium yoelii
   Q7RQ77 PLAYO yoelii]
                                                                      AA
                                                                      align
 Score = 40.0 \text{ bits } (92), \text{ Expect = } 0.11
 Identities = 63/259 (24%), Positives = 101/259 (38%), Gaps = 52/259 (20%)
Query: 110 KYKNDGIQNYIHNEYTIINC--MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE 167
           K N G+ H+ I NC N+ G ++I N +T+ + F+E
Sbjct: 787 KMSNWGMSLNHHDNININNCDSFSNDKGNILNINNN-----EISDNNNTNFYEEEKKI 839
Query: 168 DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEII----FKLDGDI 222
             SE I++ + T N K + K E N + +I ++ +N T+ +KLD D+
Sbjct: 840 FTSESIDKRGLIEQTQINNVTKHLYDIKKEENENYNNINDLRSNKSIVSSKFSYKLDTDV 899
Query: 223 -----DR------TQFIWMKYFSIFNTELSQSNIEERYKIQSYSE 256
                                      +F+ KY
                                                            ·+· +·
                     n
                                                N E +Q+NI
Sbjct: 900 LLKDSINFEKNDHINSLRKSNTDIIGYINKFVGSKYVEEGN-ETAQNNIRISGDTKIEDK 958
Query: 257 YLKDFWGNPLMYN-KEYYMF----NAGNKNSYIKL-KKDSPVGEILTRSKYN-----QNS 305
                 + YN K Y ME N+N KL KK+S + +T
Sbjct: 959 IIPIMNDSRNEYNIKNYSMFYGNKENNNQNHEDKLSKKESELFNCITNDIYNERKIYENE 1018
Query: 306 KYINYRDLYIGEKFIIRRK 324
            Y+N DL + EK
Sbjct: 1019 LYLNKDDLILNEKIFRDKK 1037
tr <u>Q6LFH3</u> Hypothetical protein [PFF0460w] [Plasmodium falciparum
                                                                      987
```

```
Q6LFH3 PLAF7 (isolate
                                                                    AΑ
               3D7)]
                                                                    align
 Score = 39.7 \text{ bits } (91), \text{ Expect = } 0.14
 Identities = 53/235 (22%), Positives = 96/235 (40%), Gaps = 32/235 (13%)
Query: 111 YKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS 170
          Sbjct: 177 YKNEEDCKYVINENKEINENK----EINEINDNNIYNVDDNNNKYK---YKYNNYDDNN 228
Query: 171 EYINRWFFVTITNNLNNAKIYINGKLESNTD----IKDIREVIANGE------IFK 217
               FT + NN ++Y+ K +++ D +K+ * + E
Sbjct: 229 KYYENAHFNTNNCHTNNKELYLLEKKQNDVDSLLILKNEKNYVKKKENLNNNISPSCVIN 288
Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNA 277
           DG+ +R + + + I E + EER
                                             +K +
Sbjct: 289 KDGENERNRSVSEPFIDIIKDE-EEKKKEERTSQYHNQNEIKKINQKDVSVETEFYM--- 344
Query: 278 GNKNSYIKLKKDSPVGEILTRSKYN-QNSKYINYRDLYIGEKFIIRRKSNSQSIN 331
           K+S + DS ++ +N +YIN + I K + K N + +N
Sbjct: 345 --KDSLL----DSLEKLLIKNVSFNFVRKEYINIFEDMITSKRDVTWKKNKKEMN 393
```

```
sp Q98PH2 Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17) [mtlD] 360 AA MTLD_MYCPU [Mycoplasma pulmonis] align
```

```
tr <u>Q7RQ7</u>7
               Hypothetical protein [PY01225] [Plasmodium yoelii
                                                                   3195
   Q7RQ77 PLAYO yoelii]
                                                                   AΑ
                                                                   align
 Score = 40.0 bits (92), Expect = 0.11
 Identities = 63/259 (24%), Positives = 101/259 (38%), Gaps = 52/259 (20%)
Query: 110 KYKNDGIQNYIHNEYTIINC--MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE 167
           K N G+ H+ I NC N+ G ++I N +T+ + F+E
Sbjct: 787 KMSNWGMSLNHHDNININNCDSFSNDKGNILNINNN-----EISDNNNTNFYEEEKKI 839
Query: 168 DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEII----FKLDGDI 222
           SE I++ + T N K + K E N + +I ++ +N T+ +KLD D+
Sbjct: 840 FTSESIDKRGLIEQTQINNVTKHLYDIKKEENENYNNINDLRSNKSIVSSKFSYKLDTDV 899
Query: 223 -----DR-----TQFIWMKYFSIFNTELSQSNIEERYKIQSYSE 256
                    15
                                    +E+ KY N E +O+NI + +
Sbjct: 900 LLKDSINFEKNDHINSLRKSNTDIIGYINKFVGSKYVEEGN-ETAQNNIRISGDTKIEDK 958
Query: 257 YLKDFWGNPLMYN-KEYYMF----NAGNKNSYIKL-KKDSPVGEILTRSKYN-----QNS 305
                + YN K Y ME N+N KL KK+S + +T YN
Sbjct: 959 IIPIMNDSRNEYNIKNYSMFYGNKENNNQNHEDKLSKKESELFNCITNDIYNERKIYENE 1018
Query: 306 KYINYRDLYIGEKFIIRRK 324
           Y+N DL + EK
Sbjct: 1019 LYLNKDDLILNEKIFRDKK 1037
```

```
tr <u>Q6LFH3</u> Hypothetical protein [PFF0460w] [Plasmodium falciparum
                                                                       987
    Q6LFH3 PLAF7 (isolate
                                                                        AΑ
                 3D7)]
                                                                        align
  Score = 39.7 \text{ bits } (91), \text{ Expect} = 0.14
  Identities = 53/235 (22%), Positives = 96/235 (40%), Gaps = 32/235 (13%)
 Query: 111 YKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS 170
           YKN+ Y+ NE IN K +I+ + I+ + D N K K +*YN +D *
 Sbjct: 177 YKNEEDCKYVINENKEINENK----EINEINDNNIYNVDDNNNKYK---YKYNNYDDNN 228
Query: 171 EYINRWFFVTITNNLNNAKIYINGKLESNTD----IKDIREVIANGE-----IFK 217
                FT + NN ++Y+ K +++ D +K+ * + E
 Sbjct: 229 KYYENAHFNTNNCHTNNKELYLLEKKQNDVDSLLILKNEKNYVKKKENLNNNISPSCVIN 288
 Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNA 277
            DG+ +R + + + T E + EER
                                                +K +
 Sbjct: 289 KDGENERNRSVSEPFIDIIKDE-EEKKKEERTSQYHNQNEIKKINQKDVSVETEFYM--- 344
 Query: 278 GNKNSYIKLKKDSPVGEILTRSKYN-QNSKYINYRDLYIGEKFIIRRKSNSQSIN 331
             K+S + DS ++ +N +YIN + I K + K N + +N
 Sbjct: 345 --KDSLL----DSLEKLLIKNVSFNFVRKEYINIFEDMITSKRDVTWKKNKKEMN 393
```

## sp <u>Q98PH2</u> Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17) [mtlD] 360 AA MTLD\_MYCPU [Mycoplasma pulmonis] align

```
Score = 39.3 \text{ bits } (90), \text{ Expect = } 0.19
Identities = 67/315 (21%), Positives = 123/315 (38%), Gaps = 69/315 (21%)
Query: 50 IDLSGYGAKVEVYDGVELNDK-----NQFKLTSSANSKIRVTQNQNIIFNSVFLDFSV 102
          Sbjct: 90 IGWSNLASLKKFFENVKLKEKAQIICFENGYKISSFFQSILNIDSNH-----FVNASV 142
Query: 103 SFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFE 162
           I P +K+D + Y+ + Y II KN S K++
Sbjct: 143 DKII--PNFKSDSLDVYVESYYEIILEQKNESQKKLNF------ 178
Query: 163 YNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
           N D+ YIN+ F+ N ++ I G L+ T I E + + +I+FK+
Sbjct: 179 VNYSTDLEAYINKKLFLV---NAIHSTIGYLGYLKKYT---YINEALNDQQILFKIKRLA 232
Query: 223 DRTQFIWMKYFSIFNTELSQSNIE---ERYKIQSYSEYLKDFWGNP---LMYNKEYYMFN 276
              I K + +F + +E +R+ I+ + + NP L N+ Y++
Sbjct: 233 KIINEILSKEYLLFKVDYLNDYLEKNLKRFSIKENQDLISRVARNPIQKLSKNERYFLI- 291
Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
               X +KK + +ID
                                       Y+++ + + + S QS ++ +
Sbjct: 292 -----YNLVKKHNLEIDILLEI-----YKSIFYYDNKMDKESSKIQSTIEN--K 333
Query: 337 KEDYIYLDFFNLNQE 351
                 F NL+QE
Sbjct: 334 SLAYALKKFSNLDQE 348
                                                                    2170
tr Q8ID18
               Hypothetical protein MAL13P1.349 [MAL13P1.349]
   Q8ID18 PLAF7 [Plasmodium
                                                                    AA
               falciparum (isolate 3D7)]
                                                                    <u>align</u>
Score = 39.3 \text{ bits } (90), \text{ Expect = } 0.19
Identities = 53/261 (20%), Positives = 101/261 (38%), Gaps = 50/261 (19%)
         NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXYKD-NNLIDLSGYGAKVEV 61
          N + + F+ + + N+ LI+M NK N
                                                 + NN+ +++
Sbjct: 773 NSRMIYLQKFNSNFFENNFDLIDMKNKNNINTTNNVNNMDNMNNINNINNINTTNNVNNI 832
Query: 62 YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH 121
          + LN+N +TS+ N+K + +++N + N + L
Sbjct: 833 NNVNNLNNINNSNITSNTNNKKKYDESENSLHNILLL-----K 870
Query: 122 NEYTIINCMKNNSGW---KISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
          N T+ NC+ N+ GW KI +++ ++ I +F E +DI+E I
Sbjct: 871 NFETVFNCVPND-GWITNKIDDEDENMLFYILHI----FELFVEIYEDKDINEII---- 920
Query: 179 VTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
               + N ++N +TD+K V II K+ + + KY S+
Sbjct: 921 -----IKNIVFFLN----HTDLKIFSIVT---RIIIKISQINPINRIFFNKYISVLMK 966
```

Query: 239 ELSQSNIEERYKIQSYSEYLK 259

Sbjct: 967 NFDKDRRRNIFLMLSYCKYEK 987

+ + + SY +Y K

```
Score = 39.3 \text{ bits } (90), \text{ Expect} = 0.19
 Identities = 67/315 (21%), Positives = 123/315 (38%), Gaps = 69/315 (21%)
Query: 50 IDLSGYGAKVEVYDGVELNDK-----NQFKLTSSANSKIRVTONONIIFNSVFLDFSV 102
          Sbjct: 90 IGWSNLASLKKFFENVKLKEKAQIICFENGYKISSFFQSILNIDSNH-----FVNASV 142
Query: 103 SFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFE 162
           I F +K+D + Y+ + Y II KN S K++
Sbjct: 143 DKII--PNFKSDSLDVYVESYYEIILEQKNESQKKLNF----- 178
Query: 163 YNIREDISEYINRWFFWTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
             D+ YIN+ F+ N ++ I G L+ T I E + + +I+FK+
Sbjct: 179 VNYSTDLEAYINKKLFLV---NAIHSTIGYLGYLKKYT---YINEALNDQQILFKIKRLA 232
Query: 223 DRTQFIWMKYFSIFNTELSQSNIE---ERYKIQSYSEYLKDFWGNP---LMYNKEYYMFN 276
               I K + +F + +E +R+ I+ + + ND L N+ Y++
Sbjct: 233 KIINEILSKEYLLFKVDYLNDYLEKNLKRFSIKENQDLISRVARNPIQKLSKNERYFLI- 291
Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
               X + KK + + T.F. X+ ++ + + + + S QS ++ +
Sbjct: 292 -----YNLVKKHNLEIDILLEI-----YKSIFYYDNKMDKESSKIQSTIEN--K 333
Query: 337 KEDYIYLDFFNLNQE 351
             Y
                 F NL+QE
Sbjct: 334 SLAYALKKFSNLDQE 348
tr Q8ID18
               Hypothetical protein MAL13P1.349 [MAL13P1.349]
                                                                    2170
   Q8ID18 PLAF7 [Plasmodium
                                                                    AΑ
               falciparum (isolate 3D7)]
                                                                    align
 Score = 39.3 \text{ bits } (90), \text{ Expect} = 0.19
 Identities = 53/261 (20%), Positives = 101/261 (38%), Gaps = 50/261 (19%)
          NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXXXYKD-NNLIDLSGYGAKVEV 61
          N + + F+ + + N+ LI+M NK N
                                                 + NN+ +++
Sbjct: 773 NSRMIYLQKFNSNFFENNFDLIDMKNKNNINTTNNVNNMDNMNNINNINNINTTNNVNNI 832
Query: 62 YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH 121
          + LN+ N +TS+ N+K + +++N + N + L
Sbjct: 833 NNVNNLNNINNSNITSNTNNKKKYDESENSLHNILLL-----K 870
Query: 122 NEYTIINCMKNNSGW---KISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
          N T+ NC+ N+ GW KI +++ ++ I +F E
Sbjct: 871 NFETVFNCVPND-GWITNKIDDEDENMLFYILHI----FELFVEIYEDKDINEII---- 920
Query: 179 VTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
               + N ++N +TD+K V II K+ + + KY S+
Sbjct: 921 -----IKNIVFFLN-----HTDLKIFSIVT---RIIIKISQINPINRIFFNKYISVLMK 966
Query: 239 ELSQSNIEERYKIQSYSEYLK 259
            + + + \times \times \times \times
Sbjct: 967 NFDKDRRRNIFLMLSYCKYEK 987
```

Wallclock time: 8 seconds

```
Database: EXPASY/UniProtKB
    Posted date: May 10, 2005 1:53 PM
 Number of letters in database: 613,355,151
 Number of sequences in database: 1,906,987
Lambda
          K
                H
   0.319
          0.138
                    0.414
Gapped
Lambda
          K
   0.267
          0.0410
                    0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 465
length of database: 613,355,151
effective HSP length: 129
effective length of query: 336
effective length of database: 367,353,828
effective search space: 123430886208
effective search space used: 123430886208
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 76 (33.9 bits)
```

ExPASy Home page Site Map Search ExPASy Contact us Proteomics tools Swiss-Prot

```
Database: EXPASY/UniProtKB
    Posted date: May 10, 2005 1:53 PM
  Number of letters in database: 613,355,151
  Number of sequences in database: 1,906,987
Lambda
          K
          0.138
   0.319
                     0.414
Gapped
Lambda
           K
   0.267
           0.0410
                    0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 465
length of database: 613,355,151
effective HSP length: 129
effective length of query: 336
effective length of database: 367,353,828
effective search space: 123430886208
effective search space used: 123430886208
T: 11
A: 40
X1: 16 ( 7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 76 (33.9 bits)
Wallclock time: 8 seconds
```

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